

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2003, 16:13:19 ; Search time 53 Seconds
(without alignments)
1369.939 Million cell updates/sec

Title: US-09-981-397A-16

Perfect score: 3545

Sequence: 1 MOPDMSLVNVIKMSDFLES.....ALHOCSDRLSLSLIYSON 671

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB pep:*
2: /cgn2_6/ptodata/2/pubpaa/PC1_NEM_PUB pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3545	100.0	671	US-09-981-397A-16	Sequence 16, Appl
2	3545	100.0	671	US-09-758-003-2	Sequence 2, Appl
3	3545	100.0	671	US-09-862-027-29	Sequence 29, Appl
4	2423.5	68.4	656	US-09-862-027-30	Sequence 30, Appl
5	428	12.1	497	US-09-862-027-8	Sequence 8, Appl
6	423	11.9	518	US-09-771-161A-231	Sequence 231, App
7	410.5	11.6	786	US-10-164-080-2	Sequence 2, Appl
8	410.5	11.6	786	US-10-299-327-2	Sequence 2, Appl
9	410.5	11.6	787	US-09-866-050A-134	Sequence 334, App
10	408.5	11.5	590	US-09-866-050A-409	Sequence 409, App
11	406	11.5	77	US-10-287-594-7	Sequence 512, App
12	405.5	11.4	478	US-09-866-050A-512	Sequence 512, App
13	402	11.3	77	US-10-112-793-27	Sequence 7, Appl
14	384	10.8	784	US-10-164-080-7	Sequence 27, Appl
15	375.5	10.6	536	US-09-866-050A-185	Sequence 185, App
16	371	10.5	540	US-10-118-984-2	Sequence 2, Appl
17	371	10.5	540	US-09-981-397A-14	Sequence 14, Appl
18	371	10.5	540	US-09-748-537-1	Sequence 1, Appl
19	371	10.5	540	US-09-728-721-2	Sequence 2, Appl

20	371	10.5	540	10	US-09-771-161A-184	Sequence 184, App
21	371	10.5	540	10	US-09-862-027-28	Sequence 28, Appl
22	371	10.5	540	12	US-10-133-780-1	Sequence 1, Appl
23	371	10.5	540	12	US-10-105-931-2	Sequence 2, Appl
24	371	10.5	544	10	US-09-925-301-1015	Sequence 1015, App
25	364	10.3	257	9	US-09-823-187-46	Sequence 46, Appl
26	358.5	10.1	280	10	US-09-515-806-15	Sequence 15, Appl
27	354	10.0	300	9	US-10-118-984-4	Sequence 4, Appl
28	354	10.0	300	10	US-09-728-721-4	Sequence 4, Appl
29	354	10.0	300	12	US-10-105-931-4	Sequence 4, Appl
30	350	9.9	278	9	US-10-172-088-9	Sequence 9, Appl
31	346.5	9.8	1367	9	US-09-870-759-120	Sequence 120, App
32	337.5	9.5	507	9	US-09-977-260-2	Sequence 2, Appl
33	337.5	9.5	507	9	US-09-977-261-2	Sequence 2, Appl
34	337.5	9.5	507	10	US-09-977-269-2	Sequence 2, Appl
35	335	9.4	370	10	US-09-205-658-107	Sequence 107, App
36	335	9.4	370	10	US-09-844-353A-107	Sequence 107, App
37	335	9.4	512	9	US-09-977-260-16	Sequence 16, Appl
38	335	9.4	512	9	US-09-977-261-16	Sequence 16, Appl
39	335	9.4	512	10	US-09-977-269-16	Sequence 16, Appl
40	323.5	9.1	450	9	US-09-977-260-7	Sequence 7, Appl
41	323.5	9.1	450	9	US-09-977-261-7	Sequence 7, Appl
42	323.5	9.1	450	9	US-10-059-585-42	Sequence 42, Appl
43	323.5	9.1	450	10	US-09-977-269-7	Sequence 7, Appl
44	321.5	9.1	258	10	US-09-840-704-3	Sequence 3, Appl
45	321.5	9.1	509	9	US-09-977-260-18	Sequence 18, Appl

ALIGNMENTS

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RESULT 1
US-09-981-397A-16
; Sequence 16, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axixma Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Mathias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and the
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981,397A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/240,750
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-397A-16
Query Match 100.0% Score 3545; DB 9; Length 671;
Best Local Similarity 100.0% Pred. No. 5.9e-234;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MOPDMSLVNVIKMSDFLESALDGGGKSLCFHRTOGLIMTKVKGKNCIEHNAL 60
|||||
1 MOPDMSLVNVIKMSDFLESALDGGGKSLCFHRTOGLIMTKVKGKNCIEHNAL 60
|||||
61 LEEAKMNRRLRHSRVKLLGVIIIEGKSLVMEYKGNLNMHVLAKESTPLSVGRITL 120
|||||
61 LEEAKMNRRLRHSRVKLLGVIIIEGKSLVMEYKGNLNMHVLAKESTPLSVGRITL 120
|||||
61 LEEAKMNRRLRHSRVKLLGVIIIEGKSLVMEYKGNLNMHVLAKESTPLSVGRITL 120
|||||
121 EITSEMCYLRGKGVTHKLPENILVNDPHIKADLCLASFKMKSILNNEHNLREVD 180
|||||
121 EITSEMCYLRGKGVTHKLPENILVNDPHIKADLCLASFKMKSILNNEHNLREVD 180
|||||
181 GTAKKNGCTLYVMAPEHLDVNAKPTKSDVYSFAVVMATFANKEPYEMNICEQQLMC 240
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Db      |||161 GTAKNGGTLYYMAPEHLNDYNAKPTKESDVYSFAVVLMAIFANKEPYENAICEQOLIMC 240
QY      |||241 IKSGNRPVDDITECPREIISLMKLCWEANPEARPTPGIEEKRFPFLYSOLEESVED 300
Db      |||241 IKSGNRPVDDITECPREIISLMKLCWEANPEARPTPGIEEKRFPFLYSOLEESVED 300
QY      |||301 VKSLKKEYSNENAVKRMQSLQDCVAVPSSRSNSATEPGSLHSSQGLGMPVEESMFA 360
Db      |||301 VKSLKKEYSNENAVKRMQSLQDCVAVPSSRSNSATEPGSLHSSQGLGMPVEESMFA 360
QY      |||361 PSLEHPOEENPSLSQSLQDEANHYHLYGSRMDROTQKQOPRONVAVNREERRRVSHPDF 420
Db      |||361 PSLEHPOEENPSLSQSLQDEANHYHLYGSRMDROTQKQOPRONVAVNREERRRVSHPDF 420
QY      |||421 AQRREYENFONTEGKGYSSAASHGNVHOPSGILTSQPOVLYXONNGLYSSHGFSTRPLD 480
Db      |||421 AQRREYENFONTEGKGYSSAASHGNVHOPSGILTSQPOVLYXONNGLYSSHGFSTRPLD 480
QY      |||481 PGTAGPRVWYRPIPSHMSLNINIPVETNYLGNTPMPFSSLPPTDESIRKITYNSTGIG 540
Db      |||481 PGTAGPRVWYRPIPSHMSLNINIPVETNYLGNTPMPFSSLPPTDESIRKITYNSTGIG 540
QY      |||541 IGAVNYMEIGTSSSLDSTNTNKEKEPAKYQALFDNTTSLTDKHLDPIRENLGKHMKN 600
Db      |||541 IGAVNYMEIGTSSSLDSTNTNKEKEPAKYQALFDNTTSLTDKHLDPIRENLGKHMKN 600
QY      |||601 CARLGTQSOIDELDHYERDGLKEKYOMLOKVMREGIKGATVGLAQLHQCRRID 660
Db      |||601 CARLGTQSOIDELDHYERDGLKEKYOMLOKVMREGIKGATVGLAQLHQCRRID 660
QY      |||661 LLSSLIYSON 671
Db      |||661 LLSSLIYSON 671

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RESULT 2

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US-09-758-003-2
; Sequence 2, Application US/09758003
; Patent No. US20020098522A1
; GENERAL INFORMATION:

```

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APPLICANT: BAICHMAL, VIJAY R

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HOANG, JIANNING

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HSU, HAILING

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GOEDEL, DAVID V

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TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
ASSAYS

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NUMBER OF SEQUENCES: 2

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CORRESPONDENCE ADDRESS:

```

```

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

```

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STREET: 75 DENISE DRIVE

```

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CITY: HILLSBOROUGH

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```

STATE: CALIFORNIA

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```

COUNTRY: USA

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ZIP: 94010

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COMPUTER READABLE FORM:

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MEDIUM TYPE: floppy disk

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OPERATING SYSTEM: IBM PC compatible

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SOFTWARE: Patentin Release #1.0, Version #1.30

```

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CURRENT APPLICATION DATA:

```

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APPLICATION NUMBER: US/09/758,003

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FILING DATE: 09-Jan-2001

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CLASSIFICATION: <Unknown>

```

```

PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: 09/132,118

```

```

FILING DATE: <Unknown>

```

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ATTORNEY/AGENT INFORMATION:

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NAME: OSMAN, RICHARD A.

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REGISTRATION NUMBER: 36,627

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REFERENCE/DOCKET NUMBER: T95-006-1

```

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; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 671 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-758-003-2

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```

Query Match      100.0%; Score 3545; DB 10; Length 671;
Best Local Similarity 100.0%; Pred. No. 5,9e-234;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MOPDMSLVNKKSSDFLESALDSGGGKYSLECHRTQGLMKTYYKGNCTIEHNEAL 60
Db      1 MOPDMSLVNKKSSDFLESALDSGGGKYSLECHRTQGLMKTYYKGNCTIEHNEAL 60
QY      61 LEEAKMNRRLRSRVKLLGVITIEGKYSLVMEYKEGNLMHVLKAEKSTPLSKGRITL 120
Db      61 LEEAKMNRRLRSRVKLLGVITIEGKYSLVMEYKEGNLMHVLKAEKSTPLSKGRITL 120
QY      121 EIEGMCYLHGKGVYHMDLKEENILVDNDFHIKTLADGLASFMMKSKLNDEHNELEVED 180
Db      121 EIEGMCYLHGKGVYHMDLKEENILVDNDFHIKTLADGLASFMMKSKLNDEHNELEVED 180
QY      181 GTAKNGGTLYYMAPEHLNDYNAKPTKESDVYSFAVVLMAIFANKEPYENAICEQOLIMC 240
Db      181 GTAKNGGTLYYMAPEHLNDYNAKPTKESDVYSFAVVLMAIFANKEPYENAICEQOLIMC 240
QY      241 IKSGNRPVDDITECPREIISLMKLCWEANPEARPTPGIEEKRFPFLYSOLEESVED 300
Db      241 IKSGNRPVDDITECPREIISLMKLCWEANPEARPTPGIEEKRFPFLYSOLEESVED 300
QY      301 VKSLKKEYSNENAVKRMQSLQDCVAVPSSRSNSATEPGSLHSSQGLGMPVEESMFA 360
Db      301 VKSLKKEYSNENAVKRMQSLQDCVAVPSSRSNSATEPGSLHSSQGLGMPVEESMFA 360
QY      361 PSLEHPOEENPSLSQSLQDEANHYHLYGSRMDROTQKQOPRONVAVNREERRRVSHPDF 420
Db      361 PSLEHPOEENPSLSQSLQDEANHYHLYGSRMDROTQKQOPRONVAVNREERRRVSHPDF 420
QY      421 AQRREYENFONTEGKGYSSAASHGNVHOPSGILTSQPOVLYXONNGLYSSHGFSTRPLD 480
Db      421 AQRREYENFONTEGKGYSSAASHGNVHOPSGILTSQPOVLYXONNGLYSSHGFSTRPLD 480
QY      481 PGTAGPRVWYRPIPSHMSLNINIPVETNYLGNTPMPFSSLPPTDESIRKITYNSTGIG 540
Db      481 PGTAGPRVWYRPIPSHMSLNINIPVETNYLGNTPMPFSSLPPTDESIRKITYNSTGIG 540
QY      541 IGAVNYMEIGTSSSLDSTNTNKEKEPAKYQALFDNTTSLTDKHLDPIRENLGKHMKN 600
Db      541 IGAVNYMEIGTSSSLDSTNTNKEKEPAKYQALFDNTTSLTDKHLDPIRENLGKHMKN 600
QY      601 CARLGTQSOIDELDHYERDGLKEKYOMLOKVMREGIKGATVGLAQLHQCRRID 660
Db      601 CARLGTQSOIDELDHYERDGLKEKYOMLOKVMREGIKGATVGLAQLHQCRRID 660
QY      661 LLSSLIYSON 671
Db      661 LLSSLIYSON 671

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RESULT 3

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US-09-862-027-29
; Sequence 29, Application US/09862027
; Patent No. US20020142428A1
; GENERAL INFORMATION:

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APPLICANT: Hodge, Martin R.

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TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof

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FILE REFERENCE: 35800/234862

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CURRENT APPLICATION NUMBER: US/09/862,027

```

CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 671
TYPE: PR1
ORGANISM: Homo sapiens
US-09-862-027-29

Query Match 100.0%; Score 3545; DB 10; Length 671;
Best Local Similarity 100.0%; Pred. No. 5,9e-234;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MOPDMSLNVIKMSDDLESNAELDSGGFGKVSICFHTQGLMIMKTYKGPNCIEHNEAL 60
QY 61 LEEAKMMNRRLRHSRVYKLLGVITIEEGKYSIVMEYMEKGNLMHYLKAEMSTPLSVKGRITL 120
DB 61 LEEAKMMNRRLRHSRVYKLLGVITIEEGKYSIVMEYMEKGNLMHYLKAEMSTPLSVKGRITL 120
QY 121 EIEEGMCLYHGKGYIHKDLKPENLVNDDEHIKTLADGLASFMMKSKLNNEHNEHLEVD 180
DB 121 EIEEGMCLYHGKGYIHKDLKPENLVNDDEHIKTLADGLASFMMKSKLNNEHNEHLEVD 180
QY 181 GTAKKNGGTYLWAPHELDVNAKPTKSDVYSFAVYLWALFANKPEYENALICEOOLIMC 240
DB 181 GTAKKNGGTYLWAPHELDVNAKPTKSDVYSFAVYLWALFANKPEYENALICEOOLIMC 240
QY 241 IKSGNRPDVEDITEYCPRETIISLMKLCWEANPEARPTFGIEEFPFYLSOLEEVEED 300
DB 241 IKSGNRPDVEDITEYCPRETIISLMKLCWEANPEARPTFGIEEFPFYLSOLEEVEED 300
QY 301 VKSLKKEYENENAVYKRMOSLODCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESMFA 360
DB 301 VKSLKKEYENENAVYKRMOSLODCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESMFA 360
QY 361 PSLHEPOEENEPISLOSLQDEANVHYLGSMDROTQOOPRONVAYNNEEERRRRVSDPF 420
DB 361 PSLHEPOEENEPISLOSLQDEANVHYLGSMDROTQOOPRONVAYNNEEERRRRVSDPF 420
QY 421 AORRYENFONTEGKGVYSSAASHGNAVHOPSGTOSPOVLYONNGLYSHGFGTRPLD 480
DB 421 AORRYENFONTEGKGVYSSAASHGNAVHOPSGTOSPOVLYONNGLYSHGFGTRPLD 480
QY 481 PGTAGPRVWYRPIPSHMPSLHNPVPEPTNYLGNTPTMPFSSLPPTDESIKYTIYNSTGIC 540
DB 481 PGTAGPRVWYRPIPSHMPSLHNPVPEPTNYLGNTPTMPFSSLPPTDESIKYTIYNSTGIC 540
QY 541 IGAVNYMEIGTSSSLDSTNTNFKKEPAKYOAFIPNTTSLDKHLDPRENLGKHWKN 600
DB 541 IGAVNYMEIGTSSSLDSTNTNFKKEPAKYOAFIPNTTSLDKHLDPRENLGKHWKN 600
QY 601 CARLGTOSQIDPIDHYERDGLKEKVVOMLQWVWREGIKATVGLAOLHOCGRID 660
DB 601 CARLGTOSQIDPIDHYERDGLKEKVVOMLQWVWREGIKATVGLAOLHOCGRID 660
QY 661 LLSLLIYVSON 671
DB 661 LLSLLIYVSON 671
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RESULT 4
US-09-862-027-30
Sequence 30, Application US/09862027
Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027

CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 656
TYPE: PR1
ORGANISM: Mus musculus
US-09-862-027-30

Query Match 68.4%; Score 2423.5; DB 10; Length 656;
Best Local Similarity 69.8%; Pred. No. 2,2e-157;
Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

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DB 1 MOPDMSLNVIKMSDDLESNAELDSGGFGKVSICFHTQGLMIMKTYKGPNCIEHNEAL 60
QY 61 LEEAKMMNRRLRHSRVYKLLGVITIEEGKYSIVMEYMEKGNLMHYLKAEMSTPLSVKGRITL 120
DB 61 LEEAKMMNRRLRHSRVYKLLGVITIEEGKYSIVMEYMEKGNLMHYLKAEMSTPLSVKGRITL 120
QY 121 EIEEGMCLYHGKGYIHKDLKPENLVNDDEHIKTLADGLASFMMKSKLNNEHNEHLEVD 180
DB 121 EIEEGMCLYHGKGYIHKDLKPENLVNDDEHIKTLADGLASFMMKSKLNNEHNEHLEVD 180
QY 181 GTAKKNGGTYLWAPHELDVNAKPTKSDVYSFAVYLWALFANKPEYENALICEOOLIMC 240
DB 181 GTAKKNGGTYLWAPHELDVNAKPTKSDVYSFAVYLWALFANKPEYENALICEOOLIMC 240
QY 240 CISKGNRPDVEDITEYCPRETIISLMKLCWEANPEARPTFGIEEFPFYLSOLEEVEE 299
DB 240 CISKGNRPDVEDITEYCPRETIISLMKLCWEANPEARPTFGIEEFPFYLSOLEEVEE 299
QY 300 DVSLKKEYENENAVYKRMOSLODCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESMFA 359
DB 300 DVSLKKEYENENAVYKRMOSLODCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESMFA 359
QY 359 SPSPEYQDENDRSDVQAKLOEASVYHAFGIFAEKOTRPOPONVAYNNEEERRRRVSDPF 418
DB 359 SPSPEYQDENDRSDVQAKLOEASVYHAFGIFAEKOTRPOPONVAYNNEEERRRRVSDPF 418
QY 419 FAOGRARENKISACARGHSDPTSTSRGIAVQOOLSWPATQ--TWNNGLYNHGFE---- 470
DB 419 FAOGRARENKISACARGHSDPTSTSRGIAVQOOLSWPATQ--TWNNGLYNHGFE---- 470
QY 480 DPGTAGPRVWYRPIPSHMPSLHNPVPEPTNYLGNTPTMPFSSLPPTDESIKYTIYNSTGIC 539
DB 480 DPGTAGPRVWYRPIPSHMPSLHNPVPEPTNYLGNTPTMPFSSLPPTDESIKYTIYNSTGIC 539
QY 539 QIGHNHYMDVGLNS---OPPNNTCKEBSRSRHQAIFDNTTSLDDEHLNPRENLGROWK 584
DB 539 QIGHNHYMDVGLNS---OPPNNTCKEBSRSRHQAIFDNTTSLDDEHLNPRENLGROWK 584
QY 600 NCARKLGFESQIDPIDHYERDGLKEKVVOMLQWVWREGIKATVGLAOLHOCGRID 659
DB 600 NCARKLGFESQIDPIDHYERDGLKEKVVOMLQWVWREGIKATVGLAOLHOCGRID 659
QY 659 NCARKLGFESQIDPIDHYERDGLKEKVVOMLQWVWREGIKATVGLAOLHOCGRID 664
DB 659 NCARKLGFESQIDPIDHYERDGLKEKVVOMLQWVWREGIKATVGLAOLHOCGRID 664
QY 660 LLSLLIYVSON 671
DB 660 LLSLLIYVSON 671
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RESULT 5
US-09-862-027-8
Sequence 8, Application US/09862027
Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027

```

; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 497
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-862-027-8

```

```

Query Match      12.1%; Score 428; DB 10; Length 497;
Best Local Similarity 25.4%; Pred. No. 2,7e-21;
Matches 144; Conservative 95; Mismatches 182; Indels 146; Gaps 22;

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OY 19 ESABL-DGGFGVSLCFHRTGOLMTKTVYKGPNCIEHNEALLBEAKMNLRLRSRYK 77
DB 1 ENOLVKGKGGFGTVPFAOHRKMG-----YVAVKIVNSKAISSREVKAMASLDNEFVLK 53
OY 78 LLGVI-----IEGKSLVMEYKGNLMHLAKESPTLSYKGRILIEIGMCYLHGK 132
DB 54 LEGVIEKVMWDDPKPALVTKFMENGLSGLLQSCPRPWLCLRLKEVVLGMFYLDQ 113
OY 133 G--VIHKDKPENILVNDNFHKKIADGLASFRRMMSKLNNEHNEELREVDGTAK-KNGGT 189
DB 114 NPVLLHRDLKPSNVLPDELHVKLADFGISTFGGSGQ-----SGTSGSGPGT 161
OY 190 IYMAPEHLNDVNAKPTKSDVYSFAVYVIMAFANKE---PYE-----NAICEQOLMCI 241
DB 162 LGYLAPELVNVRRASTASDVYSFGILMAYLAEREVELPEPSLYEAVCNRQ----- 216
OY 242 KGNRPDDVDITEYCPRE-----ITSLMKLCWANEPEARPTP---PGIEKFRPFYLSQ 292
DB 217 ---NRPSLAELPQAGPETPGLEGLELMQLCSSSPKRPSPQECLEPTDEVFQ-----M 268
OY 293 LEESVEEDVKSLLKKEYSNENAVYKRMQSLQDCVAVPSSRSNSATEQPGSLHSSQGLMG 352
DB 269 VENNNAVAISTYKDFLSOLRSSNRFE-----SIPES-----GOG 302
OY 303 PYESWPAFLSHPOEENEPISLOSLQDEANVHLGSHMDROTQKOPRONAVYNRRE-ER 411
DB 303 GTEMDFGFRRTIENQHSRNDVYSEWL-----NKLNLEEPSSVPKCPISLTK 349
OY 412 RRRVSHDPFAQORPEYENQTEGKTVYSSAASHGNNAVHOPSGLTSPQVLYONNGLYSS 471
DB 350 RSRADVEVPQA-----WTAGTSSDMAQP---PQTPETSTFRNOMPS- 389
OY 472 HGFGRPLDPGTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNTPTMPSSILPPTDESIK- 530
DB 390 -----PISTGT-----PS-----PGRGNGAEROGMMWSCRTPEPNPVTG 425
OY 531 ---YTIINSTGIQIGAVNYMEIGTSS 554
DB 426 RPLVNIYNGSGVQYGDNNYLTMOQTTA 452

```

RESULT 6

```

; Sequence 231, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273

```

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 231
; LENGTH: 518
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-771-161A-231

```

```

Query Match      11.9%; Score 423; DB 10; Length 518;
Best Local Similarity 25.3%; Pred. No. 6.2e-21;
Matches 145; Conservative 95; Mismatches 166; Indels 146; Gaps 22;

```

```

OY 14 SSDPLESREL-DGGFGVSLCFHRTGOLMTKTVYKGPNCIEHNEALLBEAKMNLRLR 72
DB 17 STEELNEOLVKGKGGFGTVPFAOHRKMG-----YVAVKIVNSKAISSREVKAMASLDN 69
OY 73 SRVVLGLVI-----IEGKSLVMEYKGNLMHLAKESPTLSYKGRILIEIGMCYLHGK 127
DB 70 EFLVRLLEGVIRKVMWDDPKPALVTKFMENGLSGLLQSCPRPWLCLRLKEVVLGMFYLDQ 129
OY 128 YLHGKG--VIHKDKPENILVNDNFHKKIADGLASFRRMMSKLNNEHNEELREVDGTAK- 184
DB 130 YLHDQNPVLLHRDLKPSNVLPDELHVKLADFGISTFGGSGQ-----SGTSGSG 177
OY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVYVIMAFANKE---PYE-----NAICEQ 236
DB 178 EPGGTGLYLAPELVNVRRASTASDVYSFGILMAYLAEREVELPEPSLYEAVCNRQ 237
OY 237 LIMCIKGNRPDDVDITEYCPRE-----ITSLMKLCWANEPEARPTP---PGIEKFRP 287
DB 238 -----NRPSLAELPQAGPETPGLEGLELMQLCSSSPKRPSPQECLEPTDEVFQ----- 288
OY 288 FYLSQLEESVEEDVKSLLKKEYSNENAVYKRMQSLQDCVAVPSSRSNSATEQPGSLHSSQ 347
DB 289 ---MVENNNAVAISTYKDFLSOLRSSNRFE-----SIPES----- 320
OY 348 GLGMPYEEWPAFLSHPOEENEPISLOSLQDEANVHLGSHMDROTQKOPRONAVYNRRE-ER 407
DB 321 --GGGTEMDFGFRRTIENQHSRNDVYSEWL-----NKLNLEEPSSVPKCPISLTK 365
OY 408 EE-ERRRVSHDPFAQORPEYENQTEGKTVYSSAASHGNNAVHOPSGLTSPQVLYONNGLYSS 466
DB 366 PSILTKRSRAOEEVPPQA-----WTAGTSSDMAQP---PQTPETSTFRNOMPS- 406
OY 467 GLVSSHGFGTRPLDPGTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNTPTMPSSILPPTD 526
DB 407 QMSR-----PISTGT-----PS-----PGRGNGAEROGMMWSCRTPEPNPVTG 441
OY 527 ESIR---YTIINSTGIQIGAVNYMEIGTSS 554
DB 442 NPVTGRPLVNIYNGSGVQYGDNNYLTMOQTTA 473

```

RESULT 7

```

; Sequence 2, Application US/10164080
; Publication No. US20030087411A1
; GENERAL INFORMATION:
; APPLICANT: BIRD, Timothy, A.
; APPLICANT: HOLLAND, Pamela, M.
; APPLICANT: PESCHON, Jacques, J.
; APPLICANT: VIRCA, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR) AND
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,959
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

```


Db 74 EMARFRYLPPVYGIQEE-PVGLVMEINETSLEKLLASE-PLPMDLRFRIVHETAVGMN 13

```

Db      297  DLAHEGEKS-----SLESKSEARPESSRLKRASAPFDNDCSLSELLSQL-DSGISO 34

```


Db 237 NRO-----RRPPLTELPDSEPTGLEGELKELMTWCHMSSEPKDRPSFODESKTNNV 288
 QY 289 YLSQLESVEEDKSLK---KEYSNENAVYKRMOSLO---LDCVAVPSSRSMSATEOPG 341
 Db 289 YI-LVDDKDAASKVYKHVLSQYRSSDTKLASRESSOKGTEVDC---PRETIYEMLD 342
 QY 342 SLHSSGLOGMGPVEESWFAFSLHEPOENEPISQSLQDEANHYLSRMDROTQOOPRQ 401
 Db 343 RLH-----LEEPS-----GSVERLISL----- 360
 QY 402 NVAYNREERRRRVSHDPFAOQRPYENPONTBEGKGTIVYSSASHGNAVHOPSGLTQO--- 458
 Db 361 -----TERRG-----KEASFGHAT--PAGTSSDTLA 384
 QY 459 --POVLXONGLXSSHGFGTRPLDPTGACRVYRPRIPSHMPSLHNPVETN----- 509
 Db 385 GTPQIHH---TLPSKGTTPRPAPFTETPGD-----PQRNCGGRNS 422
 QY 510 ---YLGNTPMPFSSLPPTDESIRYTYNSTGIGIAGAYNMEIGTSSSLDSTNNF-K 565
 Db 423 NPMYTNNAFN-PMTGL-----QST--VLNCSVOIGOHNCMSV-----QPRTAFPK 466
 QY 566 EEPFA 569
 Db 467 KEPA 470

RESULT 13
 US-10-112-793-27
 ; Sequence 27, Application US/10112793
 ; Publication No. US20020192729A1
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/112.793
 FILING DATE: 28-Mar-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/828.683A
 FILING DATE: 31-Mar-1997
 APPLICATION NUMBER: 08/625328
 FILING DATE: 1-Apr-1996
 APPLICATION NUMBER: 08/710802
 FILING DATE: 23-Sep-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Marschang, Diane L.
 REGISTRATION NUMBER: 35,600
 REFERENCE/DOCKET NUMBER: P1007P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5416
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 77 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-10-112-793-27

Query Match 11.3%; Score 402; DB 9; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.3e-20;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 590 IRENLGKHMKNKCAKLGFTQSOIDEIDHDYERDGLKEKYVOMLOKVMREGIGATVYGL 649
 Db 1 IRENLGKHMKNKCAKLGFTQSOIDEIDHDYERDGLKEKYVOMLOKVMREGIGATVYGL 60

QY 650 AQAHCSCRIDLSSL 665
 Db 61 AQAHCSCRIDLSSL 76

RESULT 14
 US-10-164-080-7
 ; Sequence 7, Application US/10164080
 ; Publication No. US20030087411A1
 ; GENERAL INFORMATION:
 APPLICANT: BIRD, Timothy, A.
 APPLICANT: HOLLAND, Pamela, M.
 APPLICANT: PESCHON, Jacques, J.
 TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR) AND
 FILE REFERENCE: 3280-B
 CURRENT APPLICATION NUMBER: US/10/164,080
 CURRENT FILING DATE: 2002-06-04
 PRIOR APPLICATION NUMBER: 60/295,959
 PRIOR FILING DATE: 2001-06-04
 PRIOR APPLICATION NUMBER: 60/334,362
 PRIOR FILING DATE: 2001-11-29
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 7
 LENGTH: 784
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-164-080-7

Query Match 10.8%; Score 384; DB 9; Length 784;
 Best Local Similarity 30.1%; Pred. No. 5e-18;
 Matches 120; Conservative 73; Mismatches 146; Indels 60; Gaps 17;

QY 14 SSDFLESALDSGFGKYSICFHRTOGLMTKT---YKPPNC-IEHNE--ALLEPKMM 67
 Db 19 AGFTGMEKVGSGFGQYKVRH---VHMKTWLAIKSPSLHVDREMEELLEBAKKM 73
 QY 68 NRLRHSRYVLLGVIIIEGKYSIVMEYMEKGNLMHYLKAAMSPRLSVYGRILIEIEGMC 127
 Db 74 EAAKFRYILPVYICRE--PVGLVMEYMETGSLLEKLASE-PLPMDLRFRIIETAVGMN 130
 QY 128 YLH--GKGYIHKDLKPEMLVNDPFIKXADLGLASFCKMWSKLNNEHNELEVDGTAKK 185
 Db 131 FLHGMARPLLHLDKPANILLDAHNVKISDPGLA-----KNGLSHSHLDMDGLF-- 182
 QY 186 NGCTLYYMAPEHLNDVNAKTEKSDVYSFAVYLMALFANKPEYENALICEQOLIMCKSCN 245
 Db 183 --CTIAYLPPERIRERKSLFDTKHDVYSFAIVMGVLTQKPPADEKNILHIVKVVKGH 240
 QY 246 RPVVDITTEYCPR---EISIMKLCWNEANPEARPTPGIEEKRPFYLSOLESEVE-- 299
 Db 241 RPELPVYCARPRACSHLRLMORWOGDRVRPPTQELTSETEDL-CEKPDDEVAKETAH 299
 QY 300 --DVKSS-----LKK-----EYSNENAVYKRMOSLOD-----CVAVPS--SRSN 334
 Db 300 DLDPVKSPPEDRSYVVARLKRAAPTFENDNYSLELLS--QLDSGVSAAYEGPEELSRSS 357
 QY 335 SATEOPGSLHSSGLOGMGPVEESWFAFSLHEPOENEPIS 373
 Db 358 SESKLPSSGSGKRLSGVSSVDASFASSRGSLSLSEFEREPS 396

RESULT 15

Query Match	10.6%	Score 375.5;	DB 9;	Length 536;
Best Local Similarity	29.8%	Pred No. 1.1e-17;		
Matches 122; Conservative	71;	Mismatches 172;	Indels 45;	Gaps 16

```

Oy 14 SDFLEASDLDSGFGKVCJCFHRTQGLMTKRT---VYKGPNC-IEHNE-ALBEAKMM 67
Db 20 AGEAGMEKESGGGGGQYVVRH-----VHKTKWLAIKCPSLHVDDBREHMLEEAKM 74
Oy 68 NLRHSHVNVLLVYLIEGKYSLMEYMEKGNLHVLAKEKSTPLSAKGIITLIEIGMC 127
Db 75 EMAKFRLLFVYIGDQ--PVGJLMEHMETGSEKLELASE-PLPWDRFRFRVHETATGVMN 133
Oy 128 YLH--GKVIHKLKCPENILVNDPFI-KTADGLSAFKMKSKLNNEHNEHLEBVDGTAK 184
Db 132 FLHCMSPLRLHLDKLPANTILLDAHVMSPFLDGLA-----KCNKSHSHDLSMDLF- 184
Oy 185 KNGGTLVYMAPEHLNDVNAKPTPEKSUVYSAVYLVMAIFANKPEYENAIICBOOLIMCTKSG 244
Db 185 -----GTIGYLPETIRKSKSLFTDKHVVYSFALYIMCVLQNPNFADKEKNILHIMKVVKG 241
Oy 245 NRPDDVDITTEYCPR--ETLSMLKLCWEANPEAKPTFGIEEKFRRFYLSQLEESVEDY 301
Db 242 HRPETLPICRPBPACASLIGLMQRCWMHADPQVRPTFGQITST-----TEDLCERKDEEV 296
Oy 302 KSLKREYSNENAVYKRMQSLDLDCAVAP-SKSNASNTEPDGSLHSSQIGLMPEVESWEA 360
Db 297 KDLAHEPEKS-----SLESKSARPESSSLKRAKSAVPPNDNCSLSELLSOLDGICPR 349
Oy 361 PSLHPQENEBESLQSLQ-ODEANYHLYG-SMDRQTOQOQPNVANYKNE 408
Db 350 RLKCGPELIRSSSECKLPSSSSGKRLSGVSVDBAFASSKRGSLSTFEFE 399

```

Search completed: June 21, 2003, 16:22:18
Job time : 55 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2003, 15:50:12 : Search time 73 Seconds
(without alignments)
1224.810 Million cell updates/sec

Title: US-09-981-397a-16
Perfect score: 3545
Sequence: 1 MOPDMSLVNFKMSDFLES.....ALHQCSDRLDLSLIYVSON 671

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3545	100.0	671	AAV78502	Human RIP-1 amino
2	3545	100.0	671	ABG16302	Novel human diagno
3	3545	100.0	671	AAAB82091	Human Receptor int
4	3545	100.0	671	ABAB83794	Human RIP. Homo s
5	3545	100.0	671	AAUB80370	Human cellular kin
6	3539	99.8	671	AAAI5461	Human receptor int
7	3513	99.1	671	AAAM4628	Human receptor int
8	2423.5	68.4	656	AAAM04627	Mouse receptor int
9	2416.5	68.2	656	AAAM0994	Human receptor int
10	1529	43.1	948	ABG16304	Novel human diagno

11	433	12.2	518	21	AAAB01524	Kinase of death (K
12	433	12.2	518	22	AAAB01526	Kinase of death (K
13	433	12.2	518	21	AAAB09430	Human kinase of de
14	433	12.2	518	22	AAAB09432	Human kinase of de
15	432	12.2	518	21	AAAB01530	Kinase of death (K
16	432	12.2	518	22	AAAB09436	Human kinase of de
17	428.5	12.1	555	22	AAAB07392	Novel central nerv
18	428	12.1	497	22	AAAB66604	Human h15590 prote
19	425	12.0	518	21	AAAB01525	Kinase of death (K
20	425	12.0	518	22	AAAB09431	Human kinase of de
21	423	11.9	427	22	AAAB93664	Human polypeptide
22	423	11.9	519	21	AAAY45042	Human Apop3 protei
23	423	11.9	519	21	AAAY45046	Human Apop3 (K50P)
24	414	11.7	420	21	AAAB01529	Kinase of death (K
25	414	11.7	420	22	AAAB09435	Human kinase of de
26	413.5	11.7	485	21	AAAB18658	A human regulator
27	410.5	11.6	786	21	AAAB69163	Amino acid sequenc
28	410.5	11.6	787	21	AAAB76079	Murine protein kin
29	410.5	11.6	787	22	AAAB56018	Skin cell protein.
30	410.5	11.6	787	23	AAAB72218	Murine protein iso
31	408.5	11.5	590	21	AAAB76123	Murine RIP protein
32	408.5	11.5	590	22	AAAB56062	Skin cell protein.
33	408.5	11.5	590	23	AAAB72262	Murine protein iso
34	408.5	11.5	763	21	AAAB79154	Mouse protein kina
35	405.5	11.4	478	22	AAAB20345	Rat RIP-3-like dea
36	405.5	11.4	478	23	AAAB72298	Rat protein isolat
37	401.5	11.3	436	21	AAAB45043	Human Apop3 (1-436
38	388.5	11.0	261	21	AAAB01527	Kinase of death (K
39	388.5	11.0	261	22	AAAB09433	Human kinase of de
40	387	10.9	784	22	AAAB94037	Human protein sequ
41	384	10.8	784	23	AAAB53291	Human polypeptide
42	377.5	10.6	437	21	AAAY45047	Human Apop3 (82-51
43	375.5	10.6	536	21	AAAB76007	Murine RIP protein
44	375.5	10.6	536	22	AAAB55946	Skin cell protein.
45	375.5	10.6	536	23	AAAB72146	Murine protein iso

ALIGNMENTS

RESULT 1	
AAV78502	standard; Protein: 671 AA.
ID	AAV78502
XX	
AC	AAV78502;
XX	
DT	05-MAY-2000 (first entry)
XX	
DE	Human RIP-1 amino acid sequence.
XX	
KW	RIP-1; RaBP; RLIP; antisense inhibitor; anti-inflammatory; cytostatic; anti-infective; diagnose; prevent; treatment; tumour formation.
XX	
OS	Homo sapiens.
XX	
PN	US6020198-A.
XX	
PD	01-FEB-2000.
XX	
PF	25-SEP-1998; 98US-0161443.
XX	
PR	25-SEP-1998; 98US-0161443.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Bennett CF, Cowsett LM;
XX	
DR	WPI: 2000-146889/13.
XX	
DR	N-PSDB: AAZ89748.
XX	
PT	Antisense inhibition of human RIP-1 expression, useful for diagnosing,
XX	preventing and treating conditions such as inflammation

PS Disclosure: Column 29-36; 26pp; English.

XX This sequence represents the human RIP-1 amino acid sequence. RIP-1 (also
CC known as RalBP1 and RLP1) is a GTPase activating protein (GAP) thought to
CC be a downstream target of Ral. The invention relates to RIP-1 antisense
CC phosphorothioate oligonucleotides with anti-infective, anti-inflammatory
CC and cytostatic activity. The oligonucleotides are RIP-1 antisense
CC inhibitors and are used in the diagnosis, prevention and treatment of
CC conditions associated with RIP-1 expression. Conditions associated with
CC RIP-1 expression include various infections, inflammation and tumour
CC formation.

XX Sequence 671 AA;

Query Match 100.0%; Score 3545; DB 21; Length 671;
Best Local Similarity 100.0%; Pred. No. 6, 4e-281;

Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MOPDMSLVNTKMKSSDFLESALDSGFGKVSICFHRTOGLMIMTKVYKGPNCIEHNEAL 60
DB 1 MOPDMSLVNTKMKSSDFLESALDSGFGKVSICFHRTOGLMIMTKVYKGPNCIEHNEAL 60
QY 61 LEEAKMMNRLRHSRVKLLGVIIIEEGKYSIVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
DB 61 LEEAKMMNRLRHSRVKLLGVIIIEEGKYSIVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
QY 121 EIIIEGMCYLHGKGVIIHKDLKPNIIIVDNDPHIKIADLGLASFPMWSKLNNEHNEALREV 180
DB 121 EIIIEGMCYLHGKGVIIHKDLKPNIIIVDNDPHIKIADLGLASFPMWSKLNNEHNEALREV 180
QY 181 GTAKKNGGTLTYMAPDEHLDVNAKPTKSDVYSFAVVLMAIFANKPEYENAIICEQLIMC 240
DB 181 GTAKKNGGTLTYMAPDEHLDVNAKPTKSDVYSFAVVLMAIFANKPEYENAIICEQLIMC 240
QY 241 IKSNGRPDVIDITEYCPREIISLMKICWANEAPRTEPGIEKRPFLSOLDESVEED 300
DB 241 IKSNGRPDVIDITEYCPREIISLMKICWANEAPRTEPGIEKRPFLSOLDESVEED 300
QY 301 VSLKKEYSNENAVYKRMOSLOLDCVAVPSRNSNATEOPGSLHSSOGIGMGVPEESWFA 360
DB 301 VSLKKEYSNENAVYKRMOSLOLDCVAVPSRNSNATEOPGSLHSSOGIGMGVPEESWFA 360
QY 361 PSLIEHPOEENPSLOSLODEANHYHLYGSRMDROTQOPROWAVANREERRRRVSHPDF 420
DB 361 PSLIEHPOEENPSLOSLODEANHYHLYGSRMDROTQOPROWAVANREERRRRVSHPDF 420
QY 421 AOOPEYENFONTEGKGVYSSAASHGNVHOPSGILTPOVYLYONNGLYSSHGCTRPDL 480
DB 421 AOOPEYENFONTEGKGVYSSAASHGNVHOPSGILTPOVYLYONNGLYSSHGCTRPDL 480
QY 481 PGTAGPRVWYRPIPSHMSLNHPIPEYENYLGNTPTMPFSSLPPTDESIRKTYINSGIO 540
DB 481 PGTAGPRVWYRPIPSHMSLNHPIPEYENYLGNTPTMPFSSLPPTDESIRKTYINSGIO 540
QY 541 IGAIVYMEIGTSSSLDSTNTNFKKEPAKYQALFDNTLTJTKHDPTEENIGKHAKN 600
DB 541 IGAIVYMEIGTSSSLDSTNTNFKKEPAKYQALFDNTLTJTKHDPTEENIGKHAKN 600
QY 601 CARLKGTFQSOIDELDHDERDGLKEKYOMLOKVMWREGIKGATVGLAQALHQCRRID 660
DB 601 CARLKGTFQSOIDELDHDERDGLKEKYOMLOKVMWREGIKGATVGLAQALHQCRRID 660
QY 661 LLSLTIYSON 671
DB 661 LLSLTIYSON 671

```

RESULT 2

ABG16302 ID ABG16302 standard; Protein: 671 AA.
XX AC ABG16302;
XX

```

DT 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #16293.
DE
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HUSE-) HUSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX N-PSDB: AAS80489.
XX
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20: SEQ ID No 46661; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 671 AA:
XX
XX Query Match 100.0%; Score 3545; DB 22; Length 671;
XX Best Local Similarity 100.0%; Pred. No. 6, 4e-281;
XX Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db      181  GTAKNGGTLTYMAPEHLNDVNAKPTKSDVYSFAVLMALFANKPEYENALICEQOLMC 240
Qy      241  IKSNRPDVIDITEYCPREIISLMKLCMEANPEARPEPGIEEFPRTYLSQLEESVED 300
Db      241  IKSNRPDVIDITEYCPREIISLMKLCMEANPEARPEPGIEEFPRTYLSQLEESVED 300
Qy      301  VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEOPGSLHSSOGILGMPVEESWFA 360
Db      301  VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEOPGSLHSSOGILGMPVEESWFA 360
Qy      361  PSLEHPOEENEPISQSLQDEANYHLVGSMDROTKOOPRONVAVNREERRRRVSHDPF 420
Db      361  PSLEHPOEENEPISQSLQDEANYHLVGSMDROTKOOPRONVAVNREERRRRVSHDPF 420
Qy      421  AQORPYNFPONTEKGTGVYSSAASHGNAVHQPGLTSQPOVLYONNGLYSHGFGTRPLD 480
Db      421  AQORPYNFPONTEKGTGVYSSAASHGNAVHQPGLTSQPOVLYONNGLYSHGFGTRPLD 480
Qy      481  PGTAGPVMYRPIPSHNPSLHNIPEPTNYLGNTPTMPFSSLPPTDESIRKTYINSTGIC 540
Db      481  PGTAGPVMYRPIPSHNPSLHNIPEPTNYLGNTPTMPFSSLPPTDESIRKTYINSTGIC 540
Qy      541  IGAYNWEIGGTSSSLDSTNTNFKKEPPAKYQALFDPNTTSLTDKHLDPIRENLGKHWN 600
Db      541  IGAYNWEIGGTSSSLDSTNTNFKKEPPAKYQALFDPNTTSLTDKHLDPIRENLGKHWN 600
Qy      601  CARLGTQSOIDIDHDYERDGLKEKYQMLQKWVAREGKGAIVYKLAQALHQCSDID 660
Db      601  CARLGTQSOIDIDHDYERDGLKEKYQMLQKWVAREGKGAIVYKLAQALHQCSDID 660
Qy      661  LLSLIYVSON 671
Db      661  LLSLIYVSON 671

```

RESULT 3
AAB82091
ID AAB82091 standard; Protein: 671 AA.

```

XX      XX      AAB82091:
XX      DT      28-JUN-2001 (first entry)
XX      DE      Human Receptor Interacting Protein, hRIP.
XX      KW      Human; Receptor Interacting Protein; hRIP; antibacterial; cytostatic;
KW      antinflammatory; gene therapy; infection; genetic disease; neoplasia;
KW      Tumour necrosis factor Receptor Associated Factor-2; TRAF2; TRADD;
KW      Tumour necrosis factor Receptor Associated Death Domain protein;
XX      inflammation; hypersensitivity.
XX      OS      Homo sapiens.
XX      FH      Key
FH      FT      Location/Qualifiers
FT      FT      1..300
FT      FT      /label= Kinase_domain
FT      FT      509..518
FT      FT      /label= alpha-delta1
FT      FT      /note= "Specifically claimed in Claim 6"
FT      FT      514..521
FT      FT      /label= alpha-delta2
FT      FT      /note= "Specifically claimed in Claim 7"
FT      FT      506..514
FT      FT      /label= alpha-delta3
FT      FT      /note= "Specifically claimed in Claim 8"
FT      FT      504..524
FT      FT      /label= alpha-delta4
FT      FT      /note= "Specifically claimed in Claim 9"
FT      FT      498..514
FT      FT      /label= alpha-delta5
FT      FT      /note= "Specifically claimed in Claim 10"
FT      FT      514..534
FT      FT      Region

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FT      FT      /label= alpha-delta6
FT      FT      /note= "Specifically claimed in Claim 11"
FT      FT      513..520
FT      FT      /label= alpha-delta7
FT      FT      /note= "Specifically claimed in Claim 12"
FT      FT      508..515
FT      FT      /label= alpha-delta8
FT      FT      /note= "Specifically claimed in Claim 13"
FT      FT      512..522
FT      FT      /label= alpha-delta9
FT      FT      /note= "Specifically claimed in Claim 14"
FT      FT      423..514
FT      FT      /label= alpha-delta10
FT      FT      /note= "Specifically claimed in Claim 15"
FT      FT      423..543
FT      FT      /label= alpha-delta11
FT      FT      /note= "Specifically claimed in Claim 16"
FT      FT      423..579
FT      FT      /label= alpha-delta12
FT      FT      /note= "Specifically claimed in Claim 17"
FT      FT      423..633
FT      FT      /label= alpha-delta13
FT      FT      /note= "Specifically claimed in Claim 18"
FT      FT      423..671
FT      FT      /label= alpha-delta14
FT      FT      /note= "Specifically claimed in Claim 19"
FT      FT      514..543
FT      FT      /label= alpha-delta15
FT      FT      /note= "Specifically claimed in Claim 20"
FT      FT      514..579
FT      FT      /label= alpha-delta16
FT      FT      /note= "Specifically claimed in Claim 21"
FT      FT      514..633
FT      FT      /label= alpha-delta17
FT      FT      /note= "Specifically claimed in Claim 22"
FT      FT      514..671
FT      FT      /label= alpha-delta18
FT      FT      /note= "Specifically claimed in Claim 23"

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US6211337-B1

03-APR-2001

11-AUG-1998; 98US-0132118.

23-OCT-1995; 95US-0553727.

(TULA-) TULARIK INC.

PI Baichwal VR, Huang J, Hsu H, Goeddel DV;

DR WPI: 2001-334617/35.

DR N-PSDB: AAF86480.

PT New receptor interacting protein polypeptide having threonine in
PT position 514 useful in screening assays for agents that modulate
PT interaction of protein with its binding targets

PS Claim 24; Columns 13-16; 10pp; English.

XX The present sequence is human Receptor Interacting Protein (RIP). RIP is
CC useful in screening assays for agents that modulate the interaction of
CC RIP with its natural binding targets, especially substrates such as
CC Tumour necrosis factor Receptor Associated Factor-2 (TRAF2) and Tumour
CC necrosis factor Receptor Associated Death Domain protein (TRADD). The
CC agents are potentially useful for the treatment and diagnosis of
CC diseases, e.g. infections, genetic diseases, neoplasia, inflammation and
CC hypersensitivity.

XX Sequence 671 AA;

SO Query Match 100.0%; Score 3545; DB 22; Length 671;
Best local similarity 100.0%; Pred. No. 6,4e-281;

	Matches	671: Conservative	0: Mismatches	0: Indels	0: Gaps	0:
OY	1	MQPMDSLNVIKMKSSDFLESALDSDGGFGKVSICFHRTQGLIMKTYKGCNCEIHNAL	60			
Db	1	MQPMDSLNVIKMKSSDFLESALDSDGGFGKVSICFHRTQGLIMKTYKGCNCEIHNAL	60			
OY	61	LEAKAMNRLHRSRVKLLGVYIEEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL	120			
Db	61	LEAKAMNRLHRSRVKLLGVYIEEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL	120			
OY	121	ETIEGMCYLGKGVYIHKDKPENLIVNDPFIKIADGLASFCKMWSKLNNEHNELREVD	180			
Db	121	ETIEGMCYLGKGVYIHKDKPENLIVNDPFIKIADGLASFCKMWSKLNNEHNELREVD	180			
OY	181	GTAKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMALFANKPEYENALICEQOLIMC	240			
Db	181	GTAKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMALFANKPEYENALICEQOLIMC	240			
OY	241	IKSGNRPDVDDITEYCPREIISLMKLCWEANPEARPPPGIEEKRFPYLSQLEESVED	300			
Db	241	IKSGNRPDVDDITEYCPREIISLMKLCWEANPEARPPPGIEEKRFPYLSQLEESVED	300			
OY	301	VKSLLKKESENNAVYKRMQSILQDCVAVPSSRSNSATQPSLSHSGGLMGPEESWFA	360			
Db	301	VKSLLKKESENNAVYKRMQSILQDCVAVPSSRSNSATQPSLSHSGGLMGPEESWFA	360			
OY	361	PSLEHPOEENPESLQSKLODEANHYLGSRMDRQTKOOPRONVAVYNEEERRRVSHPDF	420			
Db	361	PSLEHPOEENPESLQSKLODEANHYLGSRMDRQTKOOPRONVAVYNEEERRRVSHPDF	420			
OY	421	AQORPYENFQNTGEGKTVYSSAASHGNAVHQPSCGLTSOPQVLYONNGLYSSHGFGTRPLD	480			
Db	421	AQORPYENFQNTGEGKTVYSSAASHGNAVHQPSCGLTSOPQVLYONNGLYSSHGFGTRPLD	480			
OY	481	PGTAGPRVYWRPIBPHMPSLNIPETNYLGNPTMPFSSILPDESIKTYIYNSTGIQ	540			
Db	481	PGTAGPRVYWRPIBPHMPSLNIPETNYLGNPTMPFSSILPDESIKTYIYNSTGIQ	540			
OY	541	IGAVNYMEIGTSSSLDSTNTNFKKEPAKYQAFDMTSTLTDKHLPIRENIGKMHKN	600			
Db	541	IGAVNYMEIGTSSSLDSTNTNFKKEPAKYQAFDMTSTLTDKHLPIRENIGKMHKN	600			
OY	601	CARKIGTQSOIDELIDHDYERDGLKEKYOMLQKVMREGIKGATVGLAQLHQCNRID	660			
Db	601	CARKIGTQSOIDELIDHDYERDGLKEKYOMLQKVMREGIKGATVGLAQLHQCNRID	660			
OY	661	LLSSLIVYSON 671				
Db	661	LLSSLIVYSON 671				

RESULT 4
ABB83794
ID ABB83794 standard; Protein: 671 AA.

XX
03-SEP-2002 (first entry)

Human RIP.
Human, RIP; cell death protein RIP; receptor interacting protein; serine/threonine protein kinase; enzyme; immunosuppressive; cardiact; cerebroprotective; neuroprotective; antiparkinsonian; vitruclide; antiarthritic; antirheumatic; antidiabetic; dermatological; death receptor; caspase; necrosis; immune system; autoimmune disease; multiple sclerosis; diabetes; rheumatoid arthritis; infection; neurological disease; Alzheimer's disease; Parkinson's disease; viral; signal transduction.

XX
Homo sapiens.
XX
WO200236148-A2.

XX	10-MAY-2002.
PD	Best Local Similarity 100.0%; Score 3545; DB 23; Length 671;
XX	26-OCT-2001; 2001WO-EP12440.
PR	02-NOV-2000; 2000DE-1054279.
XX	(Apot-) APOTECH RES & DEV LTD.
PI	Tschopp J, Holler N;
XX	WPI: 2002-519224/55.
DR	N-PSDB: ABN81397.
XX	Use of a death receptor ligand or receptor interacting protein to induce necrotic cell death, useful for treating e.g. autoimmune disease, also their inhibitors
PS	Disclosure: Fig 7; 56pp; German.
CC	The invention relates to the use of a ligand (I) of the death receptor or its functional derivative, for inducing caspase-independent (I.e. necrotic) death (CID) in cells, especially those of the immune system. (I) are used to induce CID of peripheral blood lymphocytes, especially activated T cell for treatment of autoimmune diseases. Also CID can be inhibited by using agents (II) that bind to (I), or agents (III) that inhibit function of RIP (receptor-interacting protein), particularly for treatment of autoimmune diseases (e.g. multiple sclerosis, diabetes, lupus or rheumatoid arthritis); cardiac infarction; cerebral stroke; or neurological diseases (Alzheimer's or Parkinson's). (III) can also be used to treat diseases associated, at least in part, with pathological hypernecrosis and viral infections. The ligand modulates signal transduction through RIP or the death receptor. The present sequence is that of the human cell death protein RIP, a serine/threonine kinase, of the invention.
CC	Sequence 671 AA;
XX	
XX	Query Match 100.0%; Score 3545; DB 23; Length 671;
XX	Best Local Similarity 100.0%; Pred. No. 6.4e-281;
XX	Matches 671: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MQPMDSLNVIKMKSSDFLESALDSDGGFGKVSICFHRTQGLIMKTYKGCNCEIHNAL 60
Db	1 MQPMDSLNVIKMKSSDFLESALDSDGGFGKVSICFHRTQGLIMKTYKGCNCEIHNAL 60
OY	61 LEAKAMNRLHRSRVKLLGVYIEEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
Db	61 LEAKAMNRLHRSRVKLLGVYIEEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
OY	121 ETIEGMCYLGKGVYIHKDKPENLIVNDPFIKIADGLASFCKMWSKLNNEHNELREVD 180
Db	121 ETIEGMCYLGKGVYIHKDKPENLIVNDPFIKIADGLASFCKMWSKLNNEHNELREVD 180
OY	181 GTAKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMALFANKPEYENALICEQOLIMC 240
Db	181 GTAKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMALFANKPEYENALICEQOLIMC 240
OY	241 IKSGNRPDVDDITEYCPREIISLMKLCWEANPEARPPPGIEEKRFPYLSQLEESVED 300
Db	241 IKSGNRPDVDDITEYCPREIISLMKLCWEANPEARPPPGIEEKRFPYLSQLEESVED 300
OY	301 VKSLKKESENNAVYKRMQSILQDCVAVPSSRSNSATQPSLSHSGGLMGPEESWFA 360
Db	301 VKSLKKESENNAVYKRMQSILQDCVAVPSSRSNSATQPSLSHSGGLMGPEESWFA 360
OY	361 PSLEHPOEENPESLQSKLODEANHYLGSRMDRQTKOOPRONVAVYNEEERRRVSHPDF 420
Db	361 PSLEHPOEENPESLQSKLODEANHYLGSRMDRQTKOOPRONVAVYNEEERRRVSHPDF 420
OY	421 AQORPYENFQNTGEGKTVYSSAASHGNAVHQPSCGLTSOPQVLYONNGLYSSHGFGTRPLD 480
Db	421 AQORPYENFQNTGEGKTVYSSAASHGNAVHQPSCGLTSOPQVLYONNGLYSSHGFGTRPLD 480

QY 481 PGTAGRWYRPIPSHMPSLHNPVETNYLGTPTMPFSSLPPTDESIRKTYTYNSTGIG 540
 DB 481 PGTAGRWYRPIPSHMPSLHNPVETNYLGTPTMPFSSLPPTDESIRKTYTYNSTGIG 540
 QY 541 IGAYNMEIGTSSSLDSTNTNFKKEPPAKYOAIEDNTTSLTDKHLDPRENLGKHWKN 600
 DB 541 IGAYNMEIGTSSSLDSTNTNFKKEPPAKYOAIEDNTTSLTDKHLDPRENLGKHWKN 600
 QY 601 CARKLGFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIKGATVGLQAOLHOCSTRID 660
 DB 601 CARKLGFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIKGATVGLQAOLHOCSTRID 660
 QY 661 LLSLLIYVSON 671
 DB 661 LLSLLIYVSON 671

RESULT 5
 AAU80370
 ID AAU80370 standard; Protein; 671 AA.
 XX
 AC AAU80370;
 DT 30-JUL-2002 (first entry)
 XX
 DE Human cellular kinase RIP protein.
 XX
 KW Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;
 KM RIP; NCK-interacting kinase; MKK3; SRPK-2.
 XX
 OS Homo sapiens.
 OS
 PN EP1201765-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 15-OCT-2001; 2001EP-0124604.
 XX
 PR 16-OCT-2000; 2000US-240750P.
 XX
 PA (AXXI-) AXXIMA PHARM AG.
 XX
 PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
 DR MPI: 2002-373930/41.
 DR N-PSDB; ABK51170.
 XX
 PT Identifying agents for treatment or prevention of cytomegalovirus
 PT infection, comprises contacting test compound with cellular kinase and
 PT detecting change in cellular kinase activity -
 XX
 PS Disclosure; Page 27-28; 49pp; English.
 XX
 CC The present invention relates to a new method for identifying compounds
 CC for treating and/or preventing cytomegalovirus (CMV) infection and/or
 CC related diseases. The method of the invention comprises contacting a
 CC test compound with at least one of the cellular kinases RICK, RIP,
 CC NCK-interacting kinase, MKK3 and SRPK-2 and detecting any change in
 CC kinase activity. The method of the invention can be used to treat and/or
 CC prevent CMV infections and related diseases. Oligonucleotides that can
 CC detect the specified kinases can also be used for diagnosis of infection.
 CC The present amino acid sequence represents the human cellular kinase RIP
 CC protein of the invention, as described above.
 CC
 SQ Sequence 671 AA:
 Query Match 100.0%; Score 3545; DB 23; Length 671;
 Best local similarity 100.0%; Pred. No. 6, 4e-281;
 Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MOPDMSLNIYIKMKSSDFLESSELDSGGFGKVSICFHRTOGLMIMKTIVYKGPNCIEHNEAL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1 MOPDMSLNIYIKMKSSDFLESSELDSGGFGKVSICFHRTOGLMIMKTIVYKGPNCIEHNEAL 60
 QY 61 LEEAKMNNRLRHSRRVYKLLGVITIECKYSLWMEYMEKGNLMHYLAKEMSTPLSVKGRITL 120
 DB 61 LEEAKMNNRLRHSRRVYKLLGVITIECKYSLWMEYMEKGNLMHYLAKEMSTPLSVKGRITL 120
 QY 121 EIEEGMCYLHGKGVYIHKDLKPNILVNDPEHIKIALDLGLASFPMWSKLNNEEHNEELREVD 180
 DB 121 EIEEGMCYLHGKGVYIHKDLKPNILVNDPEHIKIALDLGLASFPMWSKLNNEEHNEELREVD 180
 QY 181 GTAKKNGGTLYYAPHELNDVNAKPTKESVYSPFAYVLAIFANKPEYENATEEQOLIMC 240
 DB 181 GTAKKNGGTLYYAPHELNDVNAKPTKESVYSPFAYVLAIFANKPEYENATEEQOLIMC 240
 QY 241 IKSGRNPDVDDITEYCPRETIISLMKLCWENPAPRPTFPIEERKFRFYLSQLESEYED 300
 DB 241 IKSGRNPDVDDITEYCPRETIISLMKLCWENPAPRPTFPIEERKFRFYLSQLESEYED 300
 QY 301 VKSLLKEYSNENAVVRKMSLOLDCVAVPSSRSNSATEOPGSLHSSOGLCMGPEESWFA 360
 DB 301 VKSLLKEYSNENAVVRKMSLOLDCVAVPSSRSNSATEOPGSLHSSOGLCMGPEESWFA 360
 QY 361 PSLFHPQEEENPESLOSXLQDEANYHLGSRMDQOTKQPPQONVAYNBEERRRRVSHDPF 420
 DB 361 PSLFHPQEEENPESLOSXLQDEANYHLGSRMDQOTKQPPQONVAYNBEERRRRVSHDPF 420
 QY 421 AOCRPYENFQNTGCKGVYSSAASHGNAVHQPGLTSQPOVLYONNGLYSSHGFGTRPLD 480
 DB 421 AOCRPYENFQNTGCKGVYSSAASHGNAVHQPGLTSQPOVLYONNGLYSSHGFGTRPLD 480
 QY 481 PGTAGRWYRPIPSHMPSLHNPVETNYLGTPTMPFSSLPPTDESIRKTYTYNSTGIG 540
 DB 481 PGTAGRWYRPIPSHMPSLHNPVETNYLGTPTMPFSSLPPTDESIRKTYTYNSTGIG 540
 QY 541 IGAYNMEIGTSSSLDSTNTNFKKEPPAKYOAIEDNTTSLTDKHLDPRENLGKHWKN 600
 DB 541 IGAYNMEIGTSSSLDSTNTNFKKEPPAKYOAIEDNTTSLTDKHLDPRENLGKHWKN 600
 QY 601 CARKLGFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIKGATVGLQAOLHOCSTRID 660
 DB 601 CARKLGFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIKGATVGLQAOLHOCSTRID 660
 QY 661 LLSLLIYVSON 671
 DB 661 LLSLLIYVSON 671

RESULT 6
 AAM15461
 ID AAM15461 standard; Protein; 671 AA.
 XX
 AC AAM15461;
 DT 20-JUL-1997 (first entry)
 XX
 DE Human receptor interaction protein.
 XX
 KW Receptor interaction protein; RIP; tumour necrosis factor;
 KW signal transduction; neoplasia; hypersensitivity; inflammation;
 KW diagnosis; therapy.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Domain 1..300
 FT /label= kinase_domain
 XX
 PN WO9715586-A1.
 XX
 PD 01-MAY-1997.
 XX
 PF 17-OCT-1996; 96WO-US16778.
 XX

Best Local Similarity 99.3%; Pred. No. 2.7e-278;
Matches 666; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

OY 1 MOPMSLVNIMKSSDLESAELDSGGGKVSICFHRQGLIMKTIVKGPNCIEHNEAL 60
DB 1 MOPMSLVNIMKSSDLESAELDSGGGKVSICFHRQGLIMKTIVKGPNCIEHNEAL 60
OY 61 LEEAKMNRRLRHSRVKLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVGRITL 120
DB 61 LEEAKMNRRLRHSRVKLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVGRITL 120
OY 121 EIEGMCYLHGKGYIHKDLKPENLVNDPFHIKIDAGLASFKMSKLNNEEHNEALREVD 180
DB 121 EIEGMCYLHGKGYIHKDLKPENLVNDPFHIKIDAGLASFKMSKLNNEEHNEALREVD 180
OY 181 GTAKKNGTLYYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKPEYENALICEQOLIMC 240
DB 181 GTAKKNGTLYYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKPEYENALICEQOLIMC 240
OY 241 IKSNGRPDVIDITEYCPREIISLMKLCMEANPEARPPFPGIEKFRPYLSOLESEVED 300
DB 241 IKSNGRPDVIDITEYCPREIISLMKLCMEANPEARPPFPGIEKFRPYLSOLESEVED 300
OY 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATPQPSLSHSGGLMGVPEESWFA 360
DB 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATPQPSLSHSGGLMGVPEESWFA 360
OY 361 PSLEHPOEENPESLOSLODEANHYLHGSMDROTQKOPRONVAVNREERRRVSHPDF 420
DB 361 PSLEHPOEENPESLOSLODEANHYLHGSMDROTQKOPRONVAVNREERRRVSHPDF 420
OY 421 AQQRPYENFQNTBEKGYIVSSASHGNVHQOSGLTSOPVLYQNNGLYSHGFTPLD 480
DB 421 AQQRPYENFQNTBEKGYIVSSASHGNVHQOSGLTSOPVLYQNNGLYSHGFTPLD 480
OY 481 PGTAGPRVWYRPIPSHMSLNIPVETNYLGNTPMPSLSPTDESIRKTYINSTGIQ 540
DB 481 PGTAGPRVWYRPIPSHMSLNIPVETNYLGNTPMPSLSPTDESIRKTYINSTGIQ 540
OY 541 IGAVNYMEIGTSSSLDSTNTNKEPAAKYQAFDNTTSLTKHLDPIENLGKHMKN 600
DB 541 IGAVNYMEIGTSSSLDSTNTNKEPAAKYQAFDNTTSLTKHLDPIENLGKHMKN 600
OY 601 CARLIGTQSOIDIDHDYERDGLKEKYOMLQKWMVEGIGKATVGLAOLHOCSSRID 660
DB 601 CARLIGTQSOIDIDHDYERDGLKEKYOMLQKWMVEGIGKATVGLAOLHOCSSRID 660
OY 661 LLSLLIYVSON 671
DB 661 LLSLLIYVSON 671

```

RESULT 8
AAW04627
ID AAW04627 standard; Protein: 656 AA.

AAW04627;

13-FEB-1997 (first entry)

Mouse receptor interacting protein.

Receptor interacting protein: RIP; cell death: apoptosis;

KW Fas; APO-1; signal transduction; cancer; gene therapy.

OS Mus sp.

Key Location/Qualifiers

FT Domain

1..300

/label=kinase_domain

/note="N-terminal Kinase domains extends from

a few residues after the N-terminal

Met residue to approx. residue 300"

FT Domain

557..656

FT /label=Death_domain

FT /note="the death domain covers the 98

FT C-terminal amino acid residues of RIP"

MO9636730-A1

21-NOV-1996.

18-APR-1996; 96WO-US05386.

18-MAY-1995; 95US-0444005.

(GENO) GEN HOSPITAL CORP.

(HARD) HARVARD COLLEGE.

Kim E, Leder P, Lee T, Seed B, Stranger BZ;

WPI: 1997-012100/01.

N-PSDB: AAT43752.

Receptor interacting protein having death and kinase domain - useful

to control diseases that involve abnormal apoptosis, and for

diagnosis and drug screening

Claim 5; Page 39-41; 64pp: English.

Mouse receptor interacting protein (RIP) (AAW04627) has an N-terminal

kinase domain and a C-terminal death domain through which RIP

interacts with the Fas/APO-1 intracellular domain (ICD). RIP

overexpression leads to cell death. The RIP amino acid sequence

was deduced from a cDNA clone (AAT43752) isolated from a mouse thymus

cDNA library. The RIP can be expressed in transformed host cells.

It is used to screen for cpds. that inhibit RIP-dependent promotion

of apoptosis or that induce RIP expression and therefore apoptosis.

RIP and anti-RIP antibodies are also useful as diagnostic reagents.

Sequence 656 AA.

Query Match 68.4%; Score 2423.5; DB 18; Length 656;
Best Local Similarity 69.8%; Pred. No. 3.6e-189;
Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

```

OY 1 MOPMSLVNIMKSSDLESAELDSGGGKVSICFHRQGLIMKTIVKGPNCIEHNEAL 60
DB 1 MOPMSLVNIMKSSDLESAELDSGGGKVSICFHRQGLIMKTIVKGPNCIEHNEAL 60
OY 61 LEEAKMNRRLRHSRVKLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVGRITL 120
DB 61 LEEAKMNRRLRHSRVKLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVGRITL 120
OY 121 EIEGMCYLHGKGYIHKDLKPENLVNDPFHIKIDAGLASFKMSKLNNEEHNEALREVD 180
DB 121 EIEGMCYLHGKGYIHKDLKPENLVNDPFHIKIDAGLASFKMSKLNNEEHNEALREVD 180
OY 181 GTAKKNGTLYYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKPEYENALICEQOLIM 239
DB 181 GTAKKNGTLYYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKPEYENALICEQOLIM 239
OY 240 CIKSGNRPDVIDITEYCPREIISLMKLCMEANPEARPPFPGIEKFRPYLSOLESEVED 299
DB 240 CIKSGNRPDVIDITEYCPREIISLMKLCMEANPEARPPFPGIEKFRPYLSOLESEVED 299
OY 300 DVSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATPQPSLSHSGGLMGVPEESWFA 359
DB 300 DVSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATPQPSLSHSGGLMGVPEESWFA 359
OY 360 APSLEHPOEENPESLOSLODEANHYLHGSMDROTQKOPRONVAVNREERRRVSHPDF 419
DB 360 APSLEHPOEENPESLOSLODEANHYLHGSMDROTQKOPRONVAVNREERRRVSHPDF 419
OY 420 FAQGRPYENFQNTBEKGYIVSSASHGNVHQOSGLTSOPVLYQNNGLYSHGFTPLD 479
DB 420 FAQGRPYENFQNTBEKGYIVSSASHGNVHQOSGLTSOPVLYQNNGLYSHGFTPLD 479

```

Db 419 FAOORARENKISAGARCHSDPSTTSRGIAVOQLSWPATQ---TWNNGLYNQHG-----470
QY 480 DPGTAGPRWYRPIPSHMSLNIPVEFNLYGNTPMPSSLPPTDESIKYITYNSTGI 539
Db 471 -GTGTGVMYPPNLSQMYSTYKTPVETNIPGSTPIPMFSGVADDLKTYIFNSGI 528
QY 540 QIGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTSTLTKHLDPIRENLGKHWK 599
Db 529 QIGNNHYMDVGLNS---QPPNNTCKEESTSRHOAIFDNTSTLDEHLNPIRENLGROWK 584
QY 600 NCARKLGTQSOIDEIDHDYERDGLKEKYQMLQKVMREGIKGATYGLAQLAHLQCSRI 659
Db 585 NCARKLGFETESQIDEIDHDYERDGLKEKYQMLQKVMREGIKGATYGLAQLAHLQCSRI 644
QY 660 DLLSLIYSON 671
Db 645 DLLNHLIRASQS 656

RESULT 9
AAM80994
ID AAM80994 standard; Protein; 656 AA.
XX
AC * AAM80994;
XX
DT 12-APR-1999 (first entry)
XX
DE Human receptor interacting factor RIP.
XX
KW Receptor interacting protein; RIP; RIP-interacting factor; RIF;
KW human; apoptosis.
XX
OS Homo sapiens.
XX
PN W09857985-A2.
XX
PD 23-DEC-1998.
XX
PF 19-JUN-1998; 98MO-US12778.
XX
PR 19-JUN-1997; 97US-0050196.
XX
PA (CHIR) CHIRON CORP.
XX
PI Shamoon B;
XX
DR WPI: 1999-093325/08.
XX
DR N-PSDB: AAV99818.
XX
PT New human RIP-interacting factor - used e.g. to treat muscle
XX
PT wasting diseases and autoimmune diseases
XX
PS Disclosure: Page 44-47; 57pp; English.
XX
CC This is the amino acid sequence of human receptor interacting
CC protein (RIP), a protein involved in the Fas-mediated cell death
CC pathway. The invention relates to a novel human RIP interacting
CC factor, RIF (see AAM80993) that is involved in the regulation of
CC programmed cell death. Modulation of RIF activity can be used to
CC induce or prevent apoptosis, e.g. for the treatment of cancer,
CC muscle wasting diseases and autoimmune diseases.
XX
SQ Sequence 656 AA.

Query Match 68.2%; Score 2416.5; DB 20; Length 656;
Best local similarity 69.6%; Pred. No. 1.3e-188;
Matches 468; Conservative 70; Mismatches 117; Indels 17; Gaps 5;

QY 1 MOPMSLVITKMKSSDLESALDSSGFGKYSLCFHRTOGLMINKTVYKGNCLIEHNEAL 60
Db 1 MOPMSLDNITKMASSDLLEKTDLDSSGFGKYSLCYHRSRGVILKKYVTGPNRAEYNEVL 60
QY 61 LEEAKMMNRLRHSRVKLLGLVIEGKYSLVMEYMEKGNLMHVLKAEKSTFLSVKGRILL 120

Db 61 LEEGKMMHRLRHSRVKLLGLVIEGKYSLVMEYMEKGNLMHVLKQIIVPLSKRITV 120
QY 121 EIEEGKMYLHGKGVITKDLKPEITLVNDNFHITADIGLASFEMSKNLNEEHNEALREVD 180
Db 121 EALEGKMYLHDKGVITKDLKPEITLVNDNFHITADIGLASFEMSKNLNEEHNEALREVD 180
QY 181 GTAKK-NGGVLXYMAPEHNDVNAKPTKSDVYSFVNLMAIIPANKEPEENALICEOQLM 239
Db 181 STTKNNNGTLLTYMAPEHNDVNAKPTKSDVYSFVNLMAIIPANKEPEENALICEOQLM 240
QY 240 CIKSGNRPVDVDTTEYCPREIISLMKLCMEANPEARPTPEIEKFRPYLSOLEEYVE 299
Db 241 CIKSGNRPVVEEILEYCPREIISLMRCWQAIPEDPPTLGEIEERFPYLSHFEYVE 300
QY 300 DYKSLKEEYENEAAYKRMQSLQDCAVPPSSKSNATQPGSLHSSQGLMGVPEESWF 359
Db 301 DVASLKEEYPPDQSPVLRMEVLQHDQVPLPPSRNS--EQPSLHSSQGLMGVPEESWF 358
QY 360 APSLEHPOEENEPSLQSLQDEANVHYLGSMDROTQOQPRONVAVNREERRRYSDHP 419
Db 359 SSSPEYFPQDENRSYQAKLQEEASTAHAFGLFAEKQTKPOPORONEAYNREERKRRYSDHP 418
QY 420 FAOQRPYENFQNTGKGVYSSAASHGNVHQPGLTSQPOVLYQNLNGLYSSHGFGTRPL 479
Db 419 FAOQARARENKISAGARCHSDPSTTSRGIAVOQLSWPATQ---TWNNGLYNQHG-----470
QY 480 DPGTAGPRWYRPIPSHMSLNIPVEFNLYGNTPMPSSLPPTDESIKYITYNSTGI 539
Db 471 -GTGTGVMYPPNLSQMYSTYKTPVETNIPGSTPIPMFSGVADDLKTYIFNSGI 528
QY 540 QIGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTSTLTKHLDPIRENLGKHWK 599
Db 529 QIGNNHYMDVGLNS---QPPNNTCKEESTSRHOAIFDNTSTLDEHLNPIRENLGROWK 584
QY 600 NCARKLGTQSOIDEIDHDYERDGLKEKYQMLQKVMREGIKGATYGLAQLAHLQCSRI 659
Db 585 NCARKLGFETESQIDEIDHDYERDGLKEKYQMLQKVMREGIKGATYGLAQLAHLQCSRI 644
QY 660 DLLSLIYSON 671
Db 645 DLLNHLIRASQS 656

RESULT 10
ABG16304
ID ABG16304 standard; Protein; 948 AA.
XX
AC ABG16304;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #16295.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US08631.
XX
PF 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.

DR N-PSDB: AAS80491.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 20; SEQ ID No 46663; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 948 AA;

Query Match 43.1%; Score 1529; DB 22; Length 948;

Best Local Similarity 59.4%; Pred. No. 9.9e-116;

Matches 340; Conservative 31; Mismatches 95; Indels 106; Gaps 16;

QY 1 MOPMSLVNFKMSDELESALDSDGFGKYSLCFHRGLOLMIMKTVKKGNCIEHNAL 60
DB 412 MOPMSLVNFKMSDELESALDSDGFGKYSLCFHRGLOLMIMKTVKKGNCIEHNAL 471
QY 61 LEEAKMNNRLHSHNVKLLGVIIIEGKYSLVMEYMEKGNLHVLAEMSTPLSVKGRITL 120
DB 472 LEEAKMNNRLHSHNVKLLGVIIIEGKYSLVMEYMEKGNLHVLAEMSTPLSVKGRITL 531
QY 121 EIIIGMCTYHKGKVIHDKPENTLVNDPHIKTA----- 155
DB 532 EIIIGMCTYHKGKVIHDKPENTLVNDPHIKMSTPLSVKGRITLEIIEGMCTYHKGKV 591
QY 156 ---DLGLAS-----FKMKSILNNEBHNELREVDGAKKNGGTLVYMAPEHLNDVAK 204
DB 592 IHHKLRKENTLVNDPHIKMKSILNNEBHNELREVDGAKKNGGTLVYMAPEHLNDVAK 651
QY 205 PTEKSDVYSFAVVLMAIFANKPEYENALICEQOLIMCISKSNRPVDVITTEKCPREITSLM 264
DB 652 PTEKSDVYSFAVVLMAIFANKPEYENALICEQOLIMCISKSNRPVDVITTEKCPREITSLM 711
QY 265 KLCHEANPEARPTTP-----GIEEKFRPPYLSQLESVEEDVKSLSKRETSN 310
DB 712 KLCHEANPEARPTTP-----GIEEKFRPPYLSQLESVEEDVKSLSKRETSN 771
QY 311 ENAVAKRMQSLQDLCAVPSR---SNSATQPGSLHSSQGLMGVSESWFAPSLSEHPOE 368
DB 772 HLVTAEKLP-----AAPRRRAPTCRTSEPOSAYLPH---LGAER---LPA--PRN 816
QY 369 ENPESLQSLQDEANVHLVSGRMDRQTKQOPRONVAVNREERRRRVSHDPAQORPYEN 428
DB 817 RRAPTCRTSEPOSAYLPHLGTAA---ERLPAAPR-----NRRAPTCR--TSEPOSAYLPH-- 865
QY 429 FQNTGEGCTYYSSAASHGNNAVHOPSGLSLTOPVLYONNGLYSSHGFGRLPDG----- 482
DB 866 -----LGTAEKLPAAAPRR--RAPTCRTSEPOSAYLPH-----LGTAAARLPAAAPRRNS 911

QY 483 -----TACPRVWYRPSPHMSPLHNIPVETN 509
DB 912 APTCRTSEPOSAYLP---HLGTAAARLPAAAPSN 940

RESULT 11

ID AAB01524 standard; Protein; 518 AA.

AC AAB01524;

DT 08-NOV-2000 (first entry)

DE Kinase of death (KOD).

XX KOD: kinase of death; programmed cell death; apoptosis; cancer;
XX autoimmune disease; stroke; Alzheimer's disease; identification.

OS Homo sapiens.

PM US6096539-A.

PD 01-AUG-2000.

PF 10-JUN-1999; 99US-0329418.

PR 10-JUN-1999; 99US-0329418.

PA (ZENE) ZENECA LTD.

PI Gomes BC, Prosser JC, Kasof GW;

DR WPI: 2000-523872/47.

DR N-PSDB: AAA47701, AAA47702.

PT New nucleic acids encoding a protein activator of apoptosis for
PT preventing, diagnosing and treating pathophysiological disorders
PT related to apoptosis

PS Claim 1; Columns 33-36; 32pp; English.

CC The kinase of death (KOD) polypeptide is integral to the activation
CC process of cellular apoptosis (programmed cell death). Apoptosis is
CC needed to orchestrate biological maintenance of an organism during
CC development as well as to preserve the normal function and fitness of
CC tissues during a normal life span. Physiological conditions which
CC result from aberrant apoptosis may be dire. Cancer and autoimmune
CC disease may result when there is too little apoptosis as well as
CC severe stroke damage or the neurodegeneration of Alzheimer's disease
CC when there is too much apoptosis. The KOD polypeptide is useful for
CC studying pathophysiological disorders related to apoptosis as well
CC as for identifying compounds that modulate biological and/or
CC pharmacological activity of the native mediator of apoptosis.

SQ Sequence 518 AA;

Query Match 12.2%; Score 433; DB 21; Length 518;

Best Local Similarity 25.5%; Pred. No. 1.8e-26;

Matches 146; Conservative 96; Mismatches 184; Indels 146; Gaps 22;

QY 14 SSDLESALD-DSGFGKYSLCFHRGLOLMIMKTVKKGNCIEHNALLEEAKMNNRLRH 72
DB 17 STEELNDELVGKGGFGTVFPAQRHKKG-----YDAVAIVTNSKALSREYKAMASLDN 69
QY 73 SRVYKLLGVI-----IEGKYSLVMEYMEKGNLHVLAEMSTPLSVKGRITLEIIEGMC 127
DB 70 EFVALRTEGVIEKVMNDQPKPALVTKFMENSGSLGDSQCPRPWPLLCRLLEKVLGMF 129
QY 128 YLHGKG--VHKDLKPENLVNDPHIKIADLGLASFAMSKLNNEBHNELREVDGTAK- 184
DB 130 YLHDQNPVLLHRDLKPSNVLLDPDELHYKLAIDFGSLTFGGSGO-----SGTSG 177
QY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANK-----PYE-----NAICQG 236

FT Misc-difference 112 decoding with AAD16312"
 FT /note- "Encoded by YGG; This occurs while decoding
 FT with AAD16313"
 FT 280..518
 FT Domain /note- "Death domain"
 XX US6267956-B1.
 PD 31-JUL-2001.
 XX 21-MAR-2000; 2000US-0531914.
 PF 10-JUN-1999; 99US-0329418.
 PR (ZENEC) ZENEC LTD.
 PA (ZENEC) ZENEC LTD.
 PI Gomes BC, Kasof GM, Prosser JC;
 XX WPI: 2001-535022/59.
 DR N-PSDB: AAD16312, AAD16313.
 XX New human protein activator protein, useful for treating dysfunctional
 PT apoptosis conditions and in screening assays to identify agonists which
 PT agonize or mimic biological and/or pharmacological activity -
 XX
 PS Claim 1; Column 33-36; 31pp; English.
 CC The invention relates to human protein activator of apoptosis and
 CC methods to identify compounds that modulate the biological and/or
 CC pharmacological activity of the activator and hence regulate
 CC apoptosis. The nucleic acid and amino acid sequences of the kinase
 CC of death (KOD) are useful for identifying compounds that modulate
 CC the biological and/or pharmacological activity of a native mediator
 CC of apoptosis, for treating dysfunctional apoptosis conditions, in
 CC screening assays to identify agonists which agonise or mimic
 CC biological and/or pharmacological activity, induce production of or
 CC prolong the biological half-life of the molecule in vivo or in vitro.
 CC The present sequence is human KOD protein activator of apoptosis.
 CC
 XX
 SO Sequence 518 AA:
 Query Match 12.2%; Score 433; DB 22; Length 518;
 Best Local Similarity 25.5%; Pred. No. 1.8e-26;
 Matches 146; Conservative 96; Mismatches 184; Indels 146; Gaps 22;
 OY 14 SSDFLSAEL-DSGFGKVSICFHRTGOLMIMKTVYKGPNCIEHNEALLEEAKMNRRLR 72
 DB 17 STEELNDELVGKGGFVFRAGHRKMG-----YDVAKIVSKAISREVKAMASLDN 69
 OY 73 SRVYKLGVI-----IEGKSYLMEYMEKGNLMHVLAKEBSTPLSYKGRITTEIEBMC 127
 DB 70 EYVRLTEGVLEKVMWDDPKPALVTKEMENGLSGLLOSQCPRWPLCLRLKEVILGMF 129
 OY 128 YLHKGK--VIHKDKPENILVNDNFHRIADLGLASFPMKSLNNEEHNELEVDGRAX- 184
 DB 130 YLHQNQNVLHRLDKPSNVLLDPELHVKLADFGSLTGQSGS-----SGTSGS 177
 OY 185 KNGSTLYMAPEHLNDVNAKPTKSDVYSFAVLAIFANKE---PYE-----NAICEQO 236
 DB 178 EPGGTLGYLAPLELVNNAKASTASDVYSGIILMAVLAIGREVELPEPSLVYAVCNMQ 237
 OY 237 LIMIKSGNRPDVDITIEYCPRE-----IISLMKLCNEANPEARTF---PGIEKFRP 287
 DB 238 -----NRPSTLAEPLQAGEETPGLEGLEKELMOLCWSSEKDRPSFOECLPKTDEVFO- 288
 OY 288 FYLSOLEESVVEEDVKSLEKESYENAVYKRMOSQLDQVAVPSSRSNATQPSLSHSQ 347
 DB 289 -----MVENNNAANASTYKDFLSQARSSNRF-----STPES----- 320
 OY 348 GLGKGPVEESWFAFSLSEHPOEENEPLOSKLQDEANYHLVGSRMDRQTKOOPRONVAVNR 407
 DB 321 --GOGGTGEMDGFRTIENQHSRNDVAVSEWL-----NKLMLLEPPSSVPPKCC 365

OY 408 EE-EERRRVSHDPFAQOKRYENFQNTBEKGTIVSSAASHGNAVHOPSLTQPOVLYONN 466
 DB 366 PSLTRKSRFAQEDQVPA-----WAGTSSSMQAP--POTPETSTFRN 406
 OY 467 GLYSHGFGTGPLDPTAGPRVWYRPIPSHMPSLHNIPEPTNYLGNTPTMPFSSLPPTD 526
 DB 407 QMPS-----PTSTGCT-----PS-----PGPRNGCAERQGNMNCRTPEP 441
 OY 527 ESIR-----YTIYNSTGIGIAYNWEIGTSS 554
 DB 442 NPVTGRPLVNIYNCSGVQVGDNNYLTMOQTFA 473
 RESULT 14
 AAE09432
 ID AAE09432 standard; Protein; 518 AA.
 XX AAE09432;
 AC AAE09432;
 XX 19-NOV-2001 (first entry)
 DT Human kinase of death (KOD) dominant negative mutant, K50R.
 XX Human: protein activator; apoptosis; kinase of death; KOD; therapy;
 KW cytosolic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN US6267956-B1.
 PD 31-JUL-2001.
 XX 21-MAR-2000; 2000US-0531914.
 PF 10-JUN-1999; 99US-0329418.
 PR (ZENEC) ZENEC LTD.
 PA Gomes BC, Kasof GM, Prosser JC;
 XX WPI: 2001-535022/59.
 DR New human protein activator protein, useful for treating dysfunctional
 PT apoptosis conditions and in screening assays to identify agonists which
 PT agonize or mimic biological and/or pharmacological activity -
 XX
 PS Disclosure; Column 37-40; 31pp; English.
 CC The invention relates to human protein activator of apoptosis and
 CC methods to identify compounds that modulate the biological and/or
 CC pharmacological activity of the activator and hence regulate
 CC apoptosis. The nucleic acid and amino acid sequences of the kinase
 CC of death (KOD) are useful for identifying compounds that modulate
 CC the biological and/or pharmacological activity of a native mediator
 CC of apoptosis, for treating dysfunctional apoptosis conditions, in
 CC screening assays to identify agonists which agonise or mimic
 CC biological and/or pharmacological activity, induce production of or
 CC prolong the biological half-life of the molecule in vivo or in vitro.
 CC The present sequence is a dominant negative mutant of human KOD
 CC protein activator of apoptosis. The lysine at position 50 of native
 CC KOD is changed to arginine in the mutant sequence.
 CC
 XX
 SO Sequence 518 AA:
 Query Match 12.2%; Score 433; DB 22; Length 518;
 Best Local Similarity 25.5%; Pred. No. 1.8e-26;
 Matches 146; Conservative 96; Mismatches 184; Indels 146; Gaps 22;
 OY 14 SSDFLSAEL-DSGFGKVSICFHRTGOLMIMKTVYKGPNCIEHNEALLEEAKMNRRLR 72
 DB 17 STEELNDELVGKGGFVFRAGHRKMG-----YDVAKIVSKAISREVKAMASLDN 69

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 25, 2003, 20:27:10 ; Search time 2042 Seconds

(without alignments)
5321.827 Million cell updates/sec

Title: US-09-981-397A-16

Perfect score: 3545

Sequence: 1 MOPDMSLVNKKMSDFLES.....ALHQCRIIDLSLLIVSON 671

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n model -DEV=yld
-Q/cgnt2.1/USFTO.spool/US09981397/runat_21062003_134007_18444/app-query.fasta.1.839
-DB-EST -OPM=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MAP -LARGEQUERY -NG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: em_estba: *
2: em_estlum: *
3: em_estlin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vit: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1528	43.1	869	9	AL521376	AL521376 AL521376
2	1470	41.5	971	9	AL545479	AL545479 AL545479
3	1278.5	36.1	931	14	B0962541	B0962541 ACENCOURT
4	1222	34.5	732	9	AU140586	AU140586 AU140586
5	1205	34.0	894	13	B1257769	B1257769 B1257769
6	1158	32.7	672	9	AL704842	AL704842 DKF2P686C
7	1156.5	32.6	812	12	BE864263	BE864263 B01505730
8	1142.5	32.2	656	14	BQ317122	BQ317122 OVO-CT038
9	1102	31.1	960	14	BQ647524	BQ647524 ACENCOURT
10	1028	29.0	775	13	B1663126	B1663126 603286738
11	1019.5	28.8	775	13	B1663126	B1663126 603286738
12	979.5	27.6	649	13	B1559218	B1559218 603240839
13	884	24.9	649	12	BG691740	BG691740 341033 BA
14	870	24.5	563	10	AW890282	AW890282 MKO-NT003
15	864.5	24.4	786	12	BG387238	BG387238 602455976
16	850	24.0	484	9	AL039269	AL039269 DKF2P7270
17	746	21.0	663	10	BE573589	BE573589 601333617
18	735	20.7	500	12	BG689507	BG689507 337612 BA
19	691	19.5	444	10	BE001662	BE001662 PMO-BN008
20	689	19.4	693	12	BF055235	BF055235 717412.x
21	681	19.2	674	10	BB616659	BB616659 BB616659
22	658.5	18.6	895	13	B1599131	B1599131 603246349
23	655	18.5	425	10	AW236421	AW236421 XM64606.x
24	648	18.3	552	12	BE756621	BE756621 210812 MA
25	639	18.0	1028	9	AL571266	AL571266 AL571266
26	635	17.9	942	10	BE285518	BE285518 601096893
27	633	17.7	385	12	BF086124	BF086124 CM2-GN005
28	627.5	17.4	409	12	BF737966	BF737966 CM2-KT003
29	625.5	17.6	585	13	BM191199	BM191199 d8133310
30	589	16.6	574	9	AA271576	AA271576 VB77407.r
31	572	16.1	707	9	AJ455969	AJ455969 AJ455969
32	493	13.9	893	13	B1331833	B1331833 6029842511
33	488.5	13.8	670	13	BJ000439	BJ000439 BJ000439
34	459	12.9	310	9	A1801478	A1801478 t089h04.x
35	455	12.8	506	10	AW433969	AW433969 UT-R-BJ09
36	436	12.3	323	10	AW353174	AW353174 34902 MAR
37	430	12.1	728	9	AL521375	AL521375 AL521375
38	424	12.0	365	10	BE381822	BE381822 601272355
39	414	11.7	483	14	B0780368	B0780368 UT-R-FE0
40	388	10.9	231	14	Z45688	Z45688 HSCZRE091.n
41	373	10.5	732	12	BE898370	BE898370 601681196
42	370	10.4	349	9	A1338106	A1338106 qtc0601.x
43	354	10.0	1051	12	BF783377	BF783377 602110215
44	340.5	9.6	305	9	AA143087	AA143087 z069b11.r
45	338.5	9.5	2046	11	AK013606	AK013606 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS AL521376
DEFINITION AL521376 LTL_NF1004_NBC2 Homo sapiens CDNA clone CSDB0001YF10 5
ACCESSION AL521376
VERSION AL521376.1 GI:12784869
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 869)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization

JOURNAL COMMENT

Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Location/Qualifiers

1. 869

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0D0101YE14"

/clone_lib="LTI_NFL004_NBC2"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@life.com" URL : http://fulllength.invitrogen.com"

BASE COUNT 268 a 198 c 222 g 181 t

ORIGIN

Alignment Scores:

Pred. No.: 5.18e-157 Length: 869
Score: 1528.00 Matches: 288
Percent Similarity: 99.65% Conservative: 1
Best Local Similarity: 99.65% Mismatches: 0
Query Match: 43.10% Indels: 0
DB: 9 Gaps: 0

US-09-981-397a-16 (1-671) x AL545479 (1-971)

180 AspGlyThrAlaAlaLysAsnGlyGlyThrLeuTyrMetAlaProGluHisLeuAsn 199
1 GACGGCAGCCGCTAAGAAAGATGGCGCCACCTCTACTCATGAGCGCCAGCAGCTGAT 60
200 AspValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValLeuTyr 219
61 GACGTCAACGCAAGCCACAGACAGATGCGATGTACAGCTTGTGCTGTACTCTGG 120
220 AlaIlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMet 239
121 GCGATATTGGAAATTAAGAGACCATATGAAATGCTATCTGTGAGCAGCAGTTGATATG 180
240 CysIleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGlu 259
181 TGCATTAATCTGGACAGCAGCCAGATGTGATGACATCACTGACTGCCCCAAGAGAA 240
260 IleIleSerLeuMetLysLeuGlyCysTyrGlnAlaAsnProGluAlaArgProThrPhePro 279
241 ATTATCAAGTCCATGAGAGCTCTGCTGGAAACGAAATCCGAGAGCTCCGCCACATTTCT 300
280 GlyIleGlnGluLysPheArgProPheTyrLeuSerGlnLeuGlnGlnGlnGlnGlnGln 299
301 GGCATTTGAGAAATTTAGGCTTTTATTTAATTAAGTCAATTAAGAAAGAGCTAGAAAG 360
300 AspValLysSerLeuLysGlyLysGlySerAsnGluAsnAlaValAlaLysArgMetGln 319
361 GACGTGAAGAGTTTAAGAAAGAGTATTCAACGAAATGCAAGTTGTGAAGAGATGAG 420
320 SerLeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGln 339
421 TCTCTTAACATTGATTGTGTGGCAGTACTCAAGCCGCTCAAAATTCAGCCACAGAACAG 480
340 ProGlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGlnGlnGlnGlnGln 359
481 CCTGGTTCACGACAGAGTTCCAGGAGCTGGAGTGGGTCTCTGTGGAGAGAGTCTCTGTTT 540

360 AlaProSerLeuGlnHisProGlnGluAsnGluProSerLeuGlnSerLysLeuGln 379
541 GCTCTTCCCTTGACACACCCACAGAGAAATGAGCCAGCTGCAAGCTTAAGTCCAA 600
380 AspGluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnPro 399
601 GACGAAGCCAACTACATCTTTATGAGCCGCAATGAGCAGGAGCAACGAAAGCAGCC 660
400 ArgGlnAsnValAlaTyrAsnArgGluGlnGluAlaGArgArgValSerHisAspPro 419
661 AGACGAATGTGCTTAAACAGAGAGAGAAAGACGACGAGGTCTCCATGACCT 720
420 PheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGlnGlyLysGlyTyrValTyr 439
721 TTTCGACAGCAAGACCTTACAGAAATTTTCAGAAATTAAGAGGAGAAAGGCACTGCTAT 780
440 SerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnPro 459
781 TCCAGTGCAGCAGCATGATGTAATGCAAGTGCAGCCAGCCCTCAGGCTCAGCAGCCACT 840
460 GlnValLeuTyrGlnAsnAsnGlyLeu 468
841 CAAGTACTGTATCAGAACAAATGATTA 867

RESULT 2
LOCUS AL545479 971 bp mRNA linear EST 16-FEB-2001
DEFINITION AL545479 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D101YE14 5
prime, mRNA sequence.

ACCESSION AL545479
VERSION AL545479.1 GI:12877960
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

JOURNAL

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Source

1. 971

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0D101YE14"

/clone_lib="LTI_NFL006.PL2"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@life.com" URL : http://fulllength.invitrogen.com"

BASE COUNT 266 a 196 c 277 g 205 t 7 others

ORIGIN

Alignment Scores:

Pred. No.: 1.5e-150 Length: 971
Score: 1470.00 Matches: 294
Percent Similarity: 97.67% Conservative: 0
Best Local Similarity: 97.67% Mismatches: 6
Query Match: 41.47% Indels: 3
DB: 9 Gaps: 0

US-09-981-397a-16 (1-671) x AL545479 (1-971)

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       71  CACACAGCAGGSCCTTGGAGGAGGAGCGAAGATGATGACACACTGAAACACAGCCGGGTG 130
OY      76  ValLysLeuLeuGluValLleIleGluGluGlyLysTyrSerLeuValMetGluTyrMet 95
       131  GTGAGCTCTGGGCGCATCATCATAGAGGAAGGAGGAACTCCGCTGGATGAGTACATG 190
OY      96  GluLysGluLysLeuMetHisValLeuLysAlaGluMetSerThrProLeuSerValLys 115
       191  GAGAGGGGCAACCTGATGACGTCGCTGAAGCCGAGATGATGACTCCGCTTCTGTAAA 250
OY     116  GLyArgLleIleLeuGluLleIleGluGlyMetCysTyrLeuHisGlyLysGlyValLle 135
       251  GGAAGGATATTTGGAAATCATTTGAAGGATGCTGCTACTTACATGGAAGGAGGCTGATA 310
OY     136  HisLysAspLeuLysProGluAsnLleLeuValAspAsnAspPheHisLleLysLleAla 155
       311  CACAGAGACCTGAAGCTGAAATATCTCTGTGATATGACTTCCACATTAAGATCGCA 370
OY     156  AspLeuGlyLeuAlaSerPheLysMetTyrSerLysLeuAsnGluGluHisAsnGlu 175
       371  GACCTCGGCTTGGCTCTTAAGATGTGAGCAAACTGAATATGAAGACACCAATGAG 430
OY     176  LeuArgGluValAspGlyThrAlaLysLysAsnGlyLysThrLeuTyrTyrMetAlaPro 195
       431  CTGAGGGAATGAGAGCGGACCGGCTAAGAGATGCGGCGGACCTCTCTACTACATGCGGCC 490
OY     196  GluHisLeuAsnAspValAsnAlaLysProThrGluLysSerAspValTyrSerPheAla 215
       491  GAGCMCTGATGATGACGTCAACGCAAGCCACAGAGAAGTGGATGCTGATGACGTTGCG- 549
OY     216  ValValLeuThrPalaLlePheHisAsnLysGluProTyrGluAsnAlaLleCysGluGln 235
       550  GTAGTACTCTGGGCGATATTGCVAAATAGAGAGCCATATGAAATGCTATCTGAGCAG 609
OY     236  GluLeuLleMetCysLleLysSerGlyAsnArgProAspValAspAspLleThrGluTyr 255
       610  CAGTGTGATATGTCATTAATAATCTGGGACACGCGCAATGTGGATGACATCAGTACGATAC 669
OY     256  CysProArgGluLleLleSerLeuMetLysLeuCysTyr- GluAlaAsnProGluAlaArg 275
       670  TGGCCAGAGAAATATATCATGCTCATGATGAGCTGTGCGGGAACGAAATCGGAAGCTCG 729
OY     275  GProThrPheProGlyLleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGlu 295
       730  GCCGACATTTCTGCGCATGTGAAGAAATTTAGGCCCTTTTATTTAAGTCAATTAGAAGA 789
OY     295  uSerValGluGluAspValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValAla 315
       790  AAGTGTGAGAGAGACGCTGAAGAGTTTAAAGAAAGATATTCAACCAAAATGAGAGTGT 849
OY     315  LlysArgMetGlnSerLeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSe 335
       850  GAGAGAGATGACAGCTCTTCAACTTGATGTGTGSGAGTACTTCAAGCCGCGTAAATTC 909
OY     335  ValThrGluGlnProGlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGlu 355
       910  AGGCACAGAACAGACT- GGTTCAGTGCACAGCTTCCAGGAGACTTGGGATGGGCKCTGTGA 968
OY     355  u 355
Db      969  G 969

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```

SOURCE
ORGANISM      human.
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rga@pds-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LCM2564 row: d column: 04
High quality sequence start: 30
High quality sequence stop: 584.

FEATURES
source
location/Qualifiers
1..931
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/clone="IMAGE:6378579"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAGCG) size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

BASE COUNT
290 a 196 c 245 g 200 t

ALIGNMENT Scores:
Pred. No.: 1,59e-129 Length: 931
Score: 1278.50 Matches: 271
Percent Similarity: 89.84% Conservative: 12
Best Local Similarity: 86.03% Mismatches: 13
Query Match: 36.06% Indels: 19
DB: 14 Gaps: 5

US-09-981-397a-16 (1-671) x B0962541 (1-931)
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       13  GACGAGGGGAGACATGCA-----GAAGGGAACCTGATGACAGCTG 51
OY     104  LeuLysAlaGluMetSerThrProLeuSerValLysGlyArgLleIleLeuGluLle 123
       52  CTGAAGCCGAGATGAGTACCTCCGCTTGTGTAAGAGGAAGATATTTGGAATGATTT 111
OY     124  GluGlyMetCysTyrLleHisGlyLysGlyValLleHisLysAspLeuLysProGluAsn 143
       112  GAAGGATGTGCTGCTTACATGGAAGAGCGCTGTATACAGAGACCTGAAGCCGTGAAT 171
OY     144  IleLeuValAspAsnAspPheHisLleLysLleAlaAspLeuGlyLeuAlaSerPheLys 163
       172  ATCTGTGTGATATGACTTCCACATTAAGATCGCAGACCTCGGCTTGCTTAAAG 231
OY     164  MetTyrSerLysLeuAsnGluGluHisAsnGluLeuArgGluValAspGlyThrAla 183
       232  ATGTGAGCAACATGAATATGAAGACACACATAGCTGAGGGAAGTGGAGCGACCGCT 291
OY     184  LysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspValAsnAla 203
       292  AAGAAGATGGCGGCGACCTCTACTACATGGCGCGCGAGACACCTGATGAGCTGACAGCA 351

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FEATURES	source
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Qy	224 AsnLysGluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCysIleLysSer 243
Db	412 AATAAGGACCAATGAATAATCCTATCTGTGAGCAGCACTTATATGTGCTAAATAATCT 471
Qy	244 GlAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIleIleSerLeu 263
Db	472 GGCACAGAGCCAGATGTGATGATCACTACTGTACTGTGCCCAAGAGAATTTCTGATCTC 531
Qy	264 MetLysLeuCysTyrGluAlaAsnProGluAlaArgProThrPheProGlyIleGluGlu 283
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Qy	303 rLeuLysLysGluTyrSerAsnGluAsnAlaValAlaVal-LysArgMetGlnSerLeuGlnL 323
Db	652 TTTAAGAAAGAGCTATTCGAAAGAAATGCACTGTGTGGAAGAAAGATGCACTGCTCTTCAAC 711
Qy	323 euAspCys-ValAlaVal-ProSerSerArgSerAsnSerAlaThrGlnGlnProGlySe 342
Db	712 TTGATTTGGGGGTGGCCATCCCTTCAAGCCGGTCAAAATTGACGACAGAAACCTCGGTTC 771
Qy	342 rLeuHisSerSer-GlnGlnLysLeuGlyMetGlyProVal---GluGlnSerTyrP---Phe 359
Db	772 CCGTCACAGTTGCCCGCAGGAGACTTGGGATTTGGGCTGTGTGCGAAGAAACCTCGGTTTGG 831
Qy	360 AlaProSer-LeuGluHisProGlnGlu---GluAsnGluProSerLeuGlnSerLysLe 378
Db	832 CTCCTCTCCCGGGGAGCACCCGCCGAGAAAGAAATGAGCCGACCTGTGCGAGAGAAAC 891
Qy	378 u---GlnAspGluAlaAsn-TyrHisLeu 386
Db	892 CTCCAAAACGAGACCACTTACCATCTTT 920
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LOCUS	AUI40586 732 bp mRNA linear EST 05-AUG-2002
DEFINITION	AUI40586 PLACE3 Homo sapiens cDNA clone PLACE3000347 5', mRNA
ACCESSION	AUI40586
KEYWORDS	AUI40586.1 GI:11002107
SOURCE	EST.
ORGANISM	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 732)
AUTHORS	Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T.,
	Nishikawa,T., Nakamura,Y., Sugano,S., Masuno,Y. and Isogai,T.
	HRI human cDNA Project (Ota,T., Suzuki,Y., Saito,K., Ishii,S.,
	Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S.,
	Masuno,Y., Isogai,T.)
TITLE	Unpublished (2000)
JOURNAL	Contact: Takao Isogai
COMMENT	Genomics Laboratory
	Helix Research Institute
	1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
	Tel: 81-438-52-3975
	Fax: 81-438-52-3986
	Email: genomcshri.co.jp
	HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
	Research Institute; cDNA library construction: Department of
	Virology, Institute of Medical Science, University of Tokyo, and
	Helix Research Institute.
	Location/Qualifiers
	1..732

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			3 others
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Score:	1222.00	Matches:	235
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Query Match:	34.47%	Indels:	1
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QY	149 Asphehisilleylslleaaspleugilyleualaserphelysmetripserlysleu	166	
Dd	62 GACTTCACAACTTAAAGATTCCGACACCTGGCCCTCCTTTAAAGATTGGAGCAACTG	121	
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QY	189 ThrLeutryTrMetalaprogLuhiSteunaspaValAsnAlalysProThrgluls	208	
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QY	289 TyrleuserglengluInguIservAlgluIsapValysSerrleuLyLysglutyr	308	
Dd	482 TAATTAAGTCAAATTAAGAAAGTGTAGACAGCGAGCTGAAGAGATTAAAGCAAAAGATAT	541	
QY	309 SerAsnGlusnaAlaValAlaylsarometginserleuglnleAsuPyValAlaVal	328	
Dd	542 TCACACGAAAATGCACTTGTGAAGAGAAATGCAAGTCTCTCAACTTGAATGTGTGGCAGTA	601	
QY	329 ProSerSarSeraSerAsnserAlathrglunglnProgliserleuHisserSergingly	348	
Dd	602 CCTTAAGCGCGTCAAATTCACGCCACAGACAGCGCTGTTACTAGCACATTTCCCANCA	661	
QY	349 LeuglymeGlyProValglungluSerttrPheAlaproSerleugluHisproglngu	368	
Dd	662 CTTCGGATGGATGCTCTGTGGANAGACTCTGGGTCTCTCTTNCCTGGAGCACCCACA -GAA	720	
QY	369 GluasngluPro 372		
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I1257769			

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DEFINITION 60296975JF1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109133 5',
mRNA sequence.
ACCESSION B1257769
VERSION B1257769.1 GI:14813469
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 894)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLMD at:
http://image.llnl.gov
Plate: L14M1264 row: f column: 14
High quality sequence stop: 738.
Location/Qualifiers
1..894
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/db_xref="taxon:9606"
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/note="Organ: cervix; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
BASE COUNT 275 a 228 c 203 g 188 t
ORIGIN
Alignment Scores:
Pred. No.: 1..8e-121 Length: 894
Score: 1205.00 Matches: 244
Percent Similarity: 94.98% Conservative: 2
Best Local Similarity: 94.21% Mismatches: 5
Query Match: 33.99% Indels: 8
DB: 13 Gaps: 0
US-09-981-397a-16 (1-671) x B1257769 (1-894)
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DB 2 AAGAGTTTAAAGAAAGAGTATCAATACGAAATGCACTTGTGAAGAAATGCACTCTCT 61
321 uGluLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnProG 341
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DB 62 TCAACTGATCTGTGTGGCAGTACTTCAAGCCGGTCAATATTCAGCCACAGAACACCTGG 121
341 ySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGlnSerTyrPheAlaPr 361
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DB 122 TTCACTGCACAGTTCGCCAGCAGCTTGGGATGGGCTCTGTGAGAGAGTGCTGTTGGCTCC 181
361 oSerLeuGlnHisProGlnGluGluAsnGlu-ProSerLeuGlnSerLysLeuGlnAspG 381
|||||
DB 182 TTCCCTGGAGCACCACCAAGAAAGAAAGACCCAGACCTCAGAGTAACTCCCAAGACG 241
381 LuAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgG 401
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OY 401 InAsnValAlaTyrAsnArgLugluGlu-ArgArgArgArgValSerHisAspProPhe 420
DB 302 AGAATGTGCTTACAAACAGAGAGAGAAACGAGACACGAGGCTCCATGACCCCTTTT 361

OY 421 AlaGlnGlnArgProTyrGluAsnPhenGlnAsnThrGluGlnGlyLysGlyThrValTyrSer 440
|||||
DB 362 GCACAGCAACAGACCTTACAGCAATTTTCAGATACAGAGGGAAGAAAGCAGCTGATATCC 421
441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
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DB 422 AGTGAGCCAGCTACTGTGAATGCGAGTGCAGCCCTCAGGCGCTCACCAGCAACCTCA 481
461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerHisGlyPheGlyThrArgProLeuAsp 480
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DB 482 GTACGTATTCAGAACAAAGGATTTATATGCTACATGGCTTTGGAACAGACCACTGGAT 541
481 ProGlyThrAlaGlyProArgValTyrTyrArgProLeuProSerHisMetProSerLeu 500
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501 HisAsnLeuProValProGluThrAsnTyrLeuGlnGlyAsnThrProThrMetProPheSer 520
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DB 602 CATATATCCACAGTCCCTGAGACACCACTATCTAGAAATACACCCACCATGCAATTCAGC 661
521 SerLeu-Pro-ProThrAspGlnSerIleLysTyrThr-IleTyrAsnSerThrGlyLe 539
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DB 662 TCCCTGACCCAGCACAACAGATGATATATATCCCAATATCAATATGACATGCGCAT 721
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OY 722 CAGATTGAGCCTTACATTAATTTGAGCTGGTGGGACC 762
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DKFZp686C1633 5', mRNA sequence.
ACCESSION AL704842
VERSION AL704842.1 GI:19688197
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 672)
Wiemann, S., Obermaier, B., Mewes, W., Mewes, H.W., Weill, B. and
Wiemann, S.
EST (Ottewaelde, B., Obermaier, B., Mewes, H.W., Weill, B. and Wiemann
, S.)
Unpublished (2001)
CONTACT: Ottewaelde B
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequencing consortium of the German Genome Project. No 5' sequence
available.
This clone (DKFZp686C1633) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..672
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp686C1633"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiIb;
cDNA-collection"
BASE COUNT 206 a 157 c 170 g 137 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 1,62e-116 Length: 672
 Score: 1158.00 Matches: 219
 Percent Similarity: 98.21% Conservative: 4
 Best Local Similarity: 98.21% Mismatches: 0
 Query Match: 32.67% Indels: 0
 DB: 9 Gaps: 0

US-09-981-397A-16 (1-671) x AL704842 (1-672)

OY 262 SerleuMetLysLeuGlySerArgMetLysPheGlnValAlaValProThrPheProGlyLeu 281
 DB 2 AGCTTCAGGAAGCTCTGCTGGAGCGCAATCCGGAAGCTCCGACATTTCTGGCATT 61
 OY 282 GluGluLysPheArgProPheThrLeuSerGlnLeuGluGluSerValGluGluAspAla 301
 DB 62 GAAGAAAATTAGGCCCTTTTATTATTAGTCATATTAGAGAAAGTGTAAGAGAGAGCCTG 121
 OY 302 LysSerLeuLysLysGluTyrSerAsnGluAsnAlaValAlaLysArgMetClnSerLeu 321
 DB 122 AAGAGTTAAAGAAAGAGTATTCAACGAAATGAGTGTGAAGAGAAAGCAGTCTT 181
 OY 322 GlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnProGly 341
 DB 182 CAACCTGATTTGTTGGCAGTACCTTCAACCGGTCAAAATTCAGCCACAGAACAGCCTGT 241
 OY 342 SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTyrPheAlaPro 361
 DB 242 TCACCTGCACAGTCTCCACAGGACCTTGGATGGCTCTGTGGAGAGATCCTGTTGCTCT 301
 OY 362 SerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAspCln 381
 DB 302 TCCCTGGAGCACCACAGAGAGAAATGAGCCAGCTCAGAGTAACCTCCAGAGAGAA 361
 OY 382 AlaAsnTyrHisLeuTyrGlySerArgMetLysPheGlnValAlaValProThrPheAlaPro 401
 DB 362 GCCAATCAACATCTTTATGAGCGCGCTGAGCAGGACGAGCAACACAGCCACAGACAG 421
 OY 402 AsnValAlaTyrAsnArgGluGluGluValArgArgValSerHisAspProPheAla 421
 DB 422 AATGTGGCTTACACAGAGAGAGAGAAAGAGAGAGGCTCCCATGAGCCTTTTCCA 481
 OY 422 GlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSerSer 441
 DB 482 CAGCAAGACCTTACGGAATTTTCAGATATACAGAGGAGAAAGCGCTTATTCAGT 541
 OY 442 AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnVal 461
 DB 542 GCACCCAGTCTGATATGAGTCCACAGCCCTCAGGCTCACCAGCCCACTCAAGTA 601
 OY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
 DB 602 CTGATATGAGAACATGATTTATATAGCCACATGCTTGGACACAGCACTGATATCA 661
 OY 482 GlyThrAla 484
 DB 662 GGAACACGA 670

RESULT 7 BE884263 812 bp mRNA linear EST 20-OCT-2000
 LOCUS BE884263
 DEFINITION 601505730F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907350 5',
 mRNA sequence.
 ACCESSION BE884263
 VERSION BE884263.1 GI:10333039
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 812)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs.rem@nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMN at:

FEATURES

Location/Qualifiers
 1..812
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3907350"
 /clone_1ib="NIH_MGC_71"
 /tissue_type="telomysarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pCMV-Sport6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.1 kb.
 High quality sequence, stop: 633.
 Plate: LAM9717 row: 1 column: 07
 http://image.llnl.gov
 Pile: LAM9717

source

BASE COUNT 259 a 195 c 190 g 168 t
 ORIGIN

Alignment Scores:

Pred. No.: 3.28e-116 Length: 812
 Score: 1156.50 Matches: 225
 Percent Similarity: 93.52% Conservative: 6
 Best Local Similarity: 91.09% Mismatches: 11
 Query Match: 32.62% Indels: 5
 DB: 12 Gaps: 1

US-09-981-397A-16 (1-671) x BE884263 (1-812)

OY 417 HisAspProPheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGly 436
 DB 3 CATGACCTCTTGGACAGCAAGACCTTACAGATTTTCAGATATACAGAGGAGAAAGGC 62
 OY 437 ThrValTyrSerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThr 456
 DB 63 ACTGCTATTCACAGTGCAGCCAGTCAAGTATGTCAGTCCAGCCAGCCCTCAGGCTCACC 122
 OY 457 SerGlnProGlnValLeuTyrGluAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThr 476
 DB 123 AGCCACCTCAAGTACTGTATACAGACATGATTTATATAGCTCAATGCTTTGGACA 182
 OY 477 ArgProLeuAspProGlyThrAlaGlyProArgValTyrPyrArgProIleProSerHis 496
 DB 183 AGACCACTGGATCCAGAGACAGAGAGGTCAGATTTGGTACAGGCCAATTCAGATCAT 242
 OY 497 MetProSerLeuHisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThr 516
 DB 243 ATGCCTAGTCTGATATATCCAGTCCAGTCCAGACCAATATACAGAAATACACCACC 302
 OY 517 MetProPheSerSerLeuProProThrAspGluSerIleLysTyrTrpIleTyrAsnSer 536
 DB 303 ATGCCATTCACTCTCTTGCACACAGATGAATCTTAATAATATACCATATACAAATAGT 362
 OY 537 ThrGlyIleGlnIleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeu 556
 DB 363 ACTGGCATTCAGATTGGAGCCTAACAATTATATGAGATTGGTGGAGAGATTCATCTCA 422
 OY 557 LeuAspSerThrAsnThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePhe 576
 DB 423 CTACACAGACCAAAATACGAATTCAGAAAGAGACCACTGCTAAGTACCAAGCATCTTT 482
 OY 577 AspaSnThrPheSerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLys 596
 DB 483 GATATATCCACTATCTGAGGATTAACCTGGAGCCCAATTCAGGAGAAATCTGGGGAAG 542
 OY 597 HisTrpLysAsnCysAlaArgLysLeu-GlyPheThrGlnSerClnIle-AspClnIleA 616

Db	543	CACGTGAAAAA	CTGTGCCCCGTTAACTGGGGCGTTCACACAGTCTCGATTTCATGTAATTTG	602
Oy	616	SPHISASPT	YGLUARqASpLYLeuLYSGlULysValTYr---GlnMetLeuGlnLYST	635
Db	603	ACCATGACTATGAGGAGAGATGTGACTGGCAAGAAAGACGGTTTACAGAGATGTCTCCAAAGT	662	
Oy	635	rp-valMet-argGluGlyIleLYSGlYAlAThYValIdLYSLysLeuAlaGlnAlaLeuHI	654	
Db	663	GGCGGATGAGACGGGAACCATACAGAGGAGCCCCGGTGGGGAAAGCTGGCGCAGGGCTCC	722	
Oy	654	gGlnCysSerArg	658	
Db	723	CCATGTTCCAGA	735	
RESULT 8				
BGI07606				
LOCUS				
DEFINITION	BGI07606	719 bp	mRNA	linear
ACCESSION	602277759p1	NIH_MGC_86	Homo sapiens	CDNA clone IMAGE:4365327 5',
VERSION	BGI07606.1	GI:12601452		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 719)			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs@mail.nih.gov			
	Tissue Procurement: ATCC			
	cDNA Library Preparation: Life Technologies, Inc.			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNL at:			
	http://image.lnl.gov			
	Plate: L1AM10014 row: f column: 16			
FEATURES	High quality sequence stop: 693.			
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	1..719			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:4365327"			
	/clone_lib="NIH_MGC_86"			
	/tissue_type="osteosarcoma, cell line"			
	/lab_host="DH10B (phage-resistant)"			
	/note="Organ: bone; Vector: pCMV-SPORT6; Site:1; NotI;			
	Site:2; SalI; Cloned unidirectionally; oligo-dt primed.			
	Average insert size 1.533 kb. Library enriched for			
	full-length clones and constructed by Life Technologies.			
	Note: this is a NIH-MGC Library."			
BASE COUNT	241 a	171 c	159 g	148 t
ORIGIN				
Alignment Scores:				
Pred. No.:	9.22e-115	Length:	719	
Score:	1142.50	Matches:	230	
Percent Similarity:	95.45%	Conservative:	1	
Best Local Similarity:	95.04%	Mismatches:	8	
Query Match:	32.23%	Indels:	6	
DB:	12	Gaps:	1	
US-09-981-397A-16 (1-671) x BGI07606 (1-719)				
Oy	396	LYSGlNGlNP	roArGlnAsnValAlaLayrAsnARgGluGluUaRGaRGaRGaVal	415
Db	2	AAACGACGACCCACAGACAGATGTGGCTTACACAACAGAGAGGAGGAAGAAGACGACGAGGTC	61	
Oy	416	SerHisAspProPheAlaGlnGlnIlaArgProTYrGluAsnPhelGlnAsnThrGluGlyLys	435	

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	SOURCE
Db	62	TOCCATGA - CCCTTTGCACACAAAGACCTTACAGAAATTTTCAGAAATACAGAGGAAAA	120				
Qy	436	GLYTHValTYrSerSerAlaAlaSerHisGlySnaIaValHisGlnProSerGlyLeu	455				
Db	121	GGAAGTGGTATTATCCAGTGCAGGACAGATCATGGTATGAGTGCAGACAGCCCTGAGGGCTC	180				
Qy	456	ThrSerGlnProGlnValLeuTYrGlnAsnAsnGlyLeuTYrSerSerHisGlyPheGly	475				
Db	181	ACAGGCCAACCTCAAGTACTGTATTCAGAACATGGATTATATACCTACATGGCTT - GGA	239				
Qy	476	ThrArgProLeuAspProGlyThAlaGlyProArgValTYrPyrArgProIleProSer	495				
Db	240	ACAAGACCACTGGATTCACGAGACAGACAGCTCCAGAGT - TGGTACAGGCCCAATTCAGT	298				
Qy	496	HisMetProSerLeuHisAsnIleProValProGluTYrLeuGlyAsnTYrPro	515				
Db	299	CATATGCCCTACTGTGCAATATATATCCAGTGGCTGTAGACCAACTATCTAGAGAAATACACC	358				
Qy	516	ThrMetProPheSerSerLeuProProThrAspGluSerIleLeuTYrTYrIleTYrAsn	535				
Db	359	ACCATGCATTCAGAGCTCCTTGCACCAACAGATGAATCTATATAATATACCATATACAT	418				
Qy	536	SerThrGlyIleGlnIleGlyAlaTYrAsnTYrMetGluIleGlyGlyTYrThrSerSerSer	555				
Db	419	AGTACTGGCATTCAGATTGGAGCCCTACAAATTATATGAGATTTGGTGGACAGTTCAATCA	478				
Qy	556	LeuLeuAspSerThrAsnTYrAsnPhelGlyGluIleProAlaIleTYrGlnAlaIle	575				
Db	479	CTACTAGACACACACAAATACGAACTTCAAAGAAAGCCAGCTGCTAAGTACCAAGCTATTC	538				
Qy	576	PheAspAsnThrThrSerLeuThrAspLYsHisLeuAspProIleArgGlu - AsnLeuG	595				
Db	539	TTGTGATATACCACTAGTCTGACGGATTAACACCTGGACCCCAATCAGGAAACATCTGGG	598				
Qy	595	LYsHisIleTYrP - LysAsnGlySnaIArgGlyLeuGlyPheThrGlnSerGlnIleAspGlu	615				
Db	599	AAAGGACACTGAAAAAACTGTCCCGTAAACCTGGGCTTCACACACTCTCAATGATGATAAA	658				
Qy	615	LeAspHisAspTYrGluArgAspGlyLeuGlySnaIValTYrGlnMetLeuGlnIleTYr	635				
Db	659	TTGACCATGACTATGAGCGAGATGGACTGAAAGAAAGGTT - --TCCAGATGTCCAAAGT	715				
Qy	635	rp 635					
Db	716	GG 717					
RESULT 9							
BO317122/c							
LOCUS	BO317122	656 bp	MRNA	linear	EST 17-MAY-2002		
DEFINITION	OVO-CT0387-180300-167-a01 CT0387	Homo sapiens	CDNA	MRNA sequence.			
ACCESSION	BO317122						
VERSION	BO317122.1	GI:20922891					
KEYWORDS	EST.						
ORGANISM	human.						
SOURCE	Homo sapiens						
REFERENCE	Emmalyrola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
	1 (bases 1 to 656)						
	Dias Neto, E., Garcia Correia, R., Verjovski-Almeida, S., Brites, M. R.,						
	Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,						
	Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bata, G. S., Simpson, D. H.,						
	Brundstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare						
	, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and						
	Simpson, A. J. G.						
	Shotgun sequencing of the human transcriptome with ORF expressed						
	sequence tags						
	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)						
	20202663						
	Contact: Simpson A.J.G.						
	Laboratory of Cancer Genetics						
	Ruwig Institute for Cancer Research						
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,						
COMMENT							

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?pl=QV0&L2=QV0-CT0387-180300-167-a01&t3=2000-03-18&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 655.

FEATURES

Source

Location/Qualifiers
1..656

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="CT0387"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site-1: Sma1; Site-2: Sma1; A mini-library was made by cloning products derived from ONESTEP PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 152 a 167 c 124 g 213 t

ORIGIN

Alignment Scores:

Pred. No.: 2,24e-110 Length: 656
Score: 1102.00 Matches: 212
Percent Similarity: 96.80% Conservative: 0
Best Local Similarity: 96.80% Mismatches: 1
Query Match: 31.09% Indels: 1
DB: 14 Gaps: 0

US-09-981-397a-16 (1-671) x BQ317122 (1-656)

107 GlnuSerThrProLeuSerValLysGlyArgIleIleLeuGluIleIleGluIleMet 126
108 GAGATGAGTACTCGGCTTCTGTAAAGAGATATTTGGAAATCATTTGAGGATG 596
127 CysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysProGluAsnIleLeuVal 146
128 TGCCTACTTACATGAAAGGCGCGGATACACAAAGACCTGAAGCCCTGAATAATTCCTTGT 536
147 AspaAspPheHisIleLysIleLeuAspLeuGlyLeuAlaSerPheLysMetTrpSer 166
148 GATATGACTCTCCAAATTAAGATGCGACACTCGGCTCTCTTAAAGTGTGGAGC 476
167 LysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAspGlyThrAlaLysLysAsn 186
168 AAACGATTAATGAAGACACATGAGCTGAGGAGAGTGGACGCGCATTAAGAAAT 416
187 GlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspValAlaAlaLysProThr 206
188 GGGGACACCTCTACTACTGAGCGCCGACGACCTGAATGAGCTAACGCAAAAGCCCA 356
207 GluLysSerAspValTyrSerPheAlaValValLeuTrpAlaIlePheAlaAsnLysGlu 226
208 GAGAAAGTCGATGTGTACAGCTTCTGTAGTACTCTGGCGCATTTTTCGAATATGAGAG 296
227 ProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCysIleLysSerGlyAsnArg 246
228 CCAATGAAAAATGCATCTGTGAGCAGCAGTTGAATATCTCATTAATCTGGCAACAG 236
247 ProAspValAspAspIleThrGluTyrCysProArgGluIleIleSerLeuMetLysLeu 266
248 CCAGATGGATGATCATCTGATGACGCGCCCAAGAGAAATTAATCATCTCATGAGCTC 176
267 CysTrpGluAlaAsnProGluAlaArgProThrPheProGlyTyrIleGluGluLysPheArg 286
268 TGCCTGGAGAGGAATCCGGAAGCTGGCGGACATTTCTGCGCATTTGAAGAAAATTTTGG 116
287 ProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspValLysSerLeuLysLys 306

115 CCTTTTAACTTAAGCATTTGAAAGAAAGTGTAAAGAGGACGCGGAGAGCTTAAAGA 56
306 SGIuTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeuGlnLeuAsp 324
55 AGAGTATTCACAAAGCAAAATGCGATTGTGTGAAGAGACAGTCTCTTCAACTTGAT 1

RESULT 10
LOCUS B0647524
DEFINITION B0647524 960 bp mRNA linear EST 15-JUL-2002
ACCESSION AGCNCOURT_8352671 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6285126
VERSION B0647524
KEYWORDS 5', mRNA sequence.
SOURCE B0647524.1 GI:21771696
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 960)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.femail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
http://image.llnl.gov
Plate: ILCM2483 row: n column: 07
High quality sequence stop: 711.

FEATURES

Source

Location/Qualifiers
1..960
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/db_xref="taxon:9606"
/clone_image="6285126"
/clone_lib="NIH-MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site-1: Xho1; Site-2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor: GCGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library."

BASE COUNT

281 a 231 c 236 g 210 t 2 others

ORIGIN

115 CCTTTTAACTTAAGCATTTGAAAGAAAGTGTAAAGAGGACGCGGAGAGCTTAAAGA 56
306 SGIuTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeuGlnLeuAsp 324
55 AGAGTATTCACAAAGCAAAATGCGATTGTGTGAAGAGACAGTCTCTTCAACTTGAT 1
US-09-981-397a-16 (1-671) x BQ647524 (1-960)
Alignment Scores:
Pred. No.: 5.92e-102 Length: 960
Score: 1028.00 Matches: 192
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.00% Indels: 0
DB: 14 Gaps: 0
480 AspProGlyThrAlaGlyProArgValTrpTyrArgProIleProSerHisMetProSer 499
14 GATCCAGACAGCAGCGATGCCAGATTGGTAACAGCCCAATCCAAATCATATGCTAGT 73
500 LeuHisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPhe 519
74 CTGCATTAATATCCAGTGGCTGTAGACCAACTATCTAGGAATAATACACCAATGCAATGC 133
520 SerSerLeuProProThrAspLysSerIleLysTyrThrIleTyrAsnSerThrGlyIle 539

Db 134 AGCTCCCTGGCCACCACAGATGATCTATAAATATCCATATACATAGTACGCATT 193
OY 540 GlnllleglYalatyAsnTYrmetGluilleglYlthrsSerSerleuAspSer 559
Db 194 CAGATTGGACCTACATATTATATGAGATTGGCGAGGATTTCATCTACTATGACAGC 253
OY 560 ThrAsnThrsAnpelysGluGluProAlaAlaLysTYrGlnAlaIleAspAsnThr 579
Db 254 ACAAAATCGAACTTCAAAGAAGACCGAGCTGCTAAGTACCAAGTACTTTGATATACC 313
OY 580 ThrSerleuThrsAspLysHsleuAspProIleargGluAsnleuGlyLysHsleu 599
Db 314 ACTAGTGTGACGATTAACACCTGGACCAATCAGGAAATCTGGGAAAGCATGGAAA 373
OY 600 AsnCysAlaArgLysleuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTYr 619
Db 374 AACTGTGCCCGTAACTGGGCTTCACACAGTCTCAGATTGATGAATTGACCATGACTAT 433
OY 620 GluArgAspLysleuYsGluYsValTYrGlnMetleuGlnYsTYrValMetArgGlu 639
Db 434 GAGCAGATGAGACTGAAAGAAAGGTTTACCAGATGCTCCAAAAGTGGTGATGAGGAA 493
OY 640 GlyIleLysGlyAlaThrValGlyLysleuAlaGlnAlaIleuHsGlnCysSerArgTle 659
Db 494 GGCATTAAGGACCCAGCGTGGGGAACCTGGCCAGCGCTCCACAGTGTTCAGAGATC 553
OY 660 AspleuLeuSerSerleuIleTYrValSerGlnAsn 671
Db 554 GACCTTCTGACAGACTTGATTACGTACGCCAGAAC 589

RESULT 11
LOCUS B1663126 775 bp mRNA linear EST 12-SEP-2001
DEFINITION 603286738F1 NCL_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5320856 5',
mpna sequence.
ACCESSION B1663126 GI:15577359
VERSION B1663126.1 GI:15577359
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 775)
TITLE NIH-MGC http://mgc.ncl.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM1813 row: 1 column: 09
High quality sequence stop: 769.
Location/Qualifiers

FEATURES

source
1..775
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5320856"
/clone_lib="NCL_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI. Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 250 a 156 c 205 g 164 t
ORIGIN
Alignment Scores:
Pred. NO.: 3.52e-101 Length: 775
Score: 1019.50 Matches: 190
Percent Similarity: 85.71% Conservative: 26
Best Local Similarity: 75.40% Mismatches: 35
Query Match: 28.76% Indels: 1
DB: 13 Gaps: 1

US-09-981-397a-16 (1-671) x B1663126 (1-775)

OY 1 MetGlnProAspMetSerleuAsnValIleLysMetLysSerSerAspPheLeuGluSer 20
Db 19 ATGCACACAGACATGCTCTTGACAAATTTAAGATGGCATCCAGTACCTGCTGGAGAG 78
OY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyCysPheHisArgThrGlnGly 40
Db 79 ACAGACCTTAGACAGCGGAGGCTTCGGAGAGGTGCTGTGTTACACAGAGGCAATGGA 138
OY 41 LeuMetLleMetLysThrValTYrLysGlyProAsnGlyIleGluHsAsnGluAlaLeu 60
Db 139 TTGTCTATCCTGAAAAAGATATACACAGGCGCCACCGCCTGAGTCAATGAGTTCTC 198
OY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValIleLysleuGly 80
Db 199 TTGGAAAGAGGGAAGATGATGACACAGCTGAGACAGCTGAGTGGTGAACCTACTGGC 258
OY 81 ValIleIleGluGluGlyLysTYrSerLeuValMetGluTYrMetGluYsGlyAsnLeu 100
Db 259 ATCATCATAGAGAGAGGAGACTATTCCTGCTGATGAGTACATGAGAGAGGCAACCTG 318
OY 101 MetHisValleuYsAlaGluMetSerThrProLeuSerValLysGlyAlaGlyIleLeu 120
Db 319 ATGCACGTGCTAAAGACCCAGATGATGTCCTCCACTTCATTTGAAAGAGGATATATCTG 378
OY 121 GluIleIleGluGluGlyMetCysTYrLeuHsGlyLysGlyValIleHisLysAspLeuLys 140
Db 379 GAGGCCATAGAGGATGCTGCTACTTACATGACAAAGTGTGATACCAAGGACCTGAG 438
OY 141 ProGluAsnIleLeuValAspAsnAspPheHisLleLysIleAlaAspLeuGlyLeuAla 160
Db 439 CCTGAGAAATATCCCTGTTGATCCGACTTTCACATTAAGATAGCCGATTTGGTGCT 498
OY 161 SerPheLysMetTrpSerLysLeuAsnGluGluHsAsnGluLeuArgGluValAsp 180
Db 499 TCCTTTAAGACATGACCAAACTGACTAAGAGAAACAACAAGAGAAAGAGTACG 558
OY 181 GlyThrAlaLysLys--AsnGlyGlyThrLeuTYrTrpMetAlaProGluHsleuAsn 199
Db 559 AGCACCCCTAGAGAGAAACATGTTGGTATACCTTTACTATGACCCGGAACACCTGAAT 618
OY 200 AspValAsnAlaLysProThrGluYsSerAspValTYrSerPheAlaValIleuTrp 219
Db 619 GACATCAATGCAAAAGCCCGAGAGAAAGTGGAGCTGTGACATTTGCTTGGCTTTGG 678
OY 220 AlaIlePheAlaAsnLysGluProTYrGluAsnAlaIleLysGluGlnGluIleMet 239
Db 679 GCAATATATTTGCAAAAAGAGCCCTTAGAGAAATCTCATCTAGCAGAGTTCGTATC 738
OY 240 CysIleLysSerGlyAsnArgProAspValAspAsp 251
Db 739 TGCAATAAATCTGTGGAGACAGGCCCAATGTAGAGGA 774

RESULT 12
LOCUS B1559218 805 bp mRNA linear EST 05-SEP-2001
DEFINITION 603240839F1 NCL_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5294000 5',
mpna sequence.
ACCESSION B1559218
VERSION B1559218.1 GI:15446532
KEYWORDS EST.

SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 805)
AUTHORS
NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rsrausb@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
Plate: LMNL1743 row: m column: 09
High quality sequence start: 4
High quality sequence stop: 775.
Location/Qualifiers
1. 805
/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:5294000"
/clone_lib="NCI CGAP_Mand"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model; Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
BASE COUNT
246 a 175 c 205 g 179 t
ORIGIN
Alignment Scores:
Pred. No.: 9.42e-97 Length: 805
Score: 979.50 Matches: 198
Percent Similarity: 82.48% Conservative: 28
Best Local Similarity: 72.26% Mismatches: 39
Query Match: 27.63% Indels: 9
DB: 13 Gaps: 2
US-09-981-397A-16 (1-671) x B1559218 (1-805)
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Db 1 CAGAAAGGCAACCGATGACGATGCTTAAGACCCAGATAGATGTCGCCCTTTCATGAAA 60
QY 116 GLYATGILEILEUGLUILEILEGLUGLYMETCYSTRYLEUHSGLYLYSGLIYVALILE 135
Db 61 GGAAGGATTAATCGTGAGGCCATAGAGGCATGTGCTACTACATGACAAAGGTGTGATA 120
QY 136 Hislyaspleuysprogluasnlleuvalaspsnaspphehisilleylileala 155
Db 121 CACAAAGGACCTGAGACCGCTGAGAAATATCTCTGTGATCTGACTTTCACATTAAATATACC 180
QY 156 Aspleuglyleualaserphelymettrpserlyseuasnaglulhisasnlu 175
Db 181 GATCTTGTTGGTCTTCTTAAACATGAGCAAACTAGACTAAGAGAAAGACAAACAG 240
QY 176 leuargluvalasp-glythratalyslys--asnlyglythrleuurytyrmetai 194
Db 241 CAGAAAGAGCTGAGCAGACCACTAGAGAACAAATGCTGTACCTTTACTACATGCGC 300
QY 194 aProgluHisleuysnspvalasnAlaLysProthgluLysSeraspvalItyrserph 214
Db 301 ACCCGAACCTGTAATGACATCAATGCAAAAGCCACGAGAAAGTGGACGTGTACAGCTT 360

QY 214 eAlavValleuTrpAlailePheAlaAsnLysgluProtyrgrluAsnAlaileCysG1 234
Db 361 TGCCATTGCTCTTTGGCGAATATTTGCAAAAAGAGCCCTTATGATGATGCTGATC 420
QY 234 uGlnGlnleuileMetCysIleLysSerGlyAsnArgProaspValasPaspIlethG1 254
Db 421 TGAGCAGTTCGTCGATGCTCATAAATCTGGAGAACGCGCAAAATGTAGAGAAATCCTTGA 480
QY 254 uTYrCysProarggluileileserleuemetLysleucysrrpAlaAsnProgluAl 274
Db 481 GTACTGTCCAAGGAGATCATGAGCTTCATGAGCGGTGCGAGCGATCCAGAAGA 540
QY 274 aArgProthrPheProgluIleGluGluLysPheArgProthryleuSerGlnleuG1 294
Db 541 CAGCGCAACATTTCTTGCCATTGAAGAAGATTAGCCCTTTTACTTAAGTCATTTTGA 600
QY 294 uGluSerValGluGluAspVal--LysSerleuysLysGluYrSerAsnGluAsnAla 313
Db 601 AGAATATGTAGAAGAGATGTGGCAGTGTGACCAAGAAAGATATCCAGATCAAGCCCA 660
QY 314 ValValLysArgMetGlnSerleuGlnleu-AspCysValAlaValProSerSer-Arg 333
Db 661 GTGCTGCAGAGAAATGTTTGACACTGCACAGCATGACTGTGTACCTCCAGACAAGGT 720
QY 333 eAsnSerAlaThrgluGlnProgluSerleuHisSerSerGlnGlyleuGlyMetGlyP 353
Db 721 CAATATCA-----GAAACACCTGATGCTGCTGCACAGCTCCAGAGGCTCCAGATGGTTC 774
QY 353 roval-GluGluSerTrpPheAlaProSer 362
Db 775 CTGTGGAGAGATCGCGGTACTTCTTC 804
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LOCUS B6691740 649 bp mRNA linear EST 02-MAY-2001
DEFINITION 341033 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION B6691740
VERSION B6691740.1 GI:13933560
KEYWORDS EST.
SOURCE
GOW, taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 649)
AUTHORS
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
Wells, K.D.
TITLE
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@nrl.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -m1nscore 18
and -m1match 12 options.
PCR primers
FORWARD: AGCAACAGCATATGACCAT
BACKWARD: GTTTCACGATCAGCAGC
Plate: 99 row: P column: 22
Seq primer: ATTAGGTGACATATG.
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1. 649
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/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;

Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT 173 a 162 c 193 g 121 t

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	2,06e-86	884.00	162	26	0	0
Percent Similarity:	89.52%					
Best Local Similarity:	77.14%					
Query Match:	24.94%					

US-09-981-397a-16 (1-671) x BG691740 (1-649)

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Oy 103 ValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeuGluIle 122
Db 19 GTGCTCAAGGCCCGGAGCATCCCTGTCGCGAAGGAGGATCATATGAGAGC 78
Oy 123 IlleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysProGlu 142
Db 79 ATCGAAGAAATCCGCTTACCTCCAGGAGAGGGGTGATACACAGGACCTCAAGCCAGAA 138
Oy 143 AsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPhe 162
Db 139 AATATCCCTGTTGACAGGAGCTTCCACATCAAGATGAGCTGGGCTGCTTCTTC 198
Oy 163 LysMetTrpSerLysLeuAsnAsnGluIuHisAsnGluLeuArgGluValAspGlyThr 182
Db 199 AAGACGTGGAGCAGCATGACGAGAGGAGACACATGACGAGGAGCGGCGGCGAGT 258
Oy 183 AlaLysLysAsnGlyLysThrLeuTyrTrpMetIleAspProGluHisLeuAsnAspValAsn 202
Db 259 GCCGGGAAGAGCGGTGGACGCTGACATGACCTGAGCCCTGAGACCTTACAGATGTAC 318
Oy 203 AlaLysProThrGluLysSerAspValTyrSerPheAlaValIleLeuTrpAlaIlePhe 222
Db 319 TCCAGGCCCTCCGAGAAGTCCGAGCTTTCAGCTTTCACATCGTCTCGGGCATCTTC 378
Oy 223 AlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGlnIleMetCysIleLys 242
Db 379 GCCAACAAGGAGCATACGAGAGCCGATGCTGTGAGCAGCATGATCTGTCATCAG 438
Oy 243 SerGlyAsnArgProAspValAspAspIleThrGluTyrGlyProArgGluIleLeuSer 262
Db 439 TCTGGGAACAGGAGCCAGAGCTGAGGACATCTTGAGTCTCCCGGGGAGTTATTTGAC 498
Oy 263 LeuMetLysLeuCysTrpGluAlaAsnProGluAlaArgProThrPheProGlyIleGlu 282
Db 499 ATCATGAGGAGCGAGTGTGAGTGAACCCGAGCAACCGCCGCTTCCGGGCAATTGAA 558
Oy 283 GluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluLysValLys 302
Db 559 GAGAAATTTAGGCTTTGATTAATCAATTTGAGAACTATGAGAGAGATGTGAAG 618
Oy 303 SerLeuLysLysGluTyrSerAsnGluAsn 312
Db 619 AGTTAAAGAAAGAGTTTCCAGGCCAATAT 648

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RESULT 14
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LOCUS M80-NT00039-010500-002-c01 NT0039 Homo sapiens CDNA, mRNA sequence.
DEFINITION AM890282
ACCESSION AM890282.1 GI:8054487
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,

TITLE
JOURNAL
MEDLINE
COMMENT
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Ancher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=st2-M80-NT0039-010500-002-c01&f3=2000-05-01&f4=1)
Seq primer: puc 18 forward
High quality sequence start: 82
High quality sequence stop: 466.
Location/Qualifiers
1..563
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/db_xref="taxon:9606"
/clone_lib="NT0039"
/dev_stage="Adult"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES

source

BASE COUNT 115 a 131 c 140 g 177 t

ALIGNMENT

Alignment Scores:
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Score: 870.00 Matches: 165
Percent Similarity: 94.38% Conservative: 3
Best Local Similarity: 92.70% Mismatches: 9
Query Match: 24.54% Indels: 1
Gaps: 0

US-09-981-397a-16 (1-671) x AM890282 (1-563)

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Oy 390 ArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArgGlu 409
Db 562 CGCATGAGCAGGACAGACAGACAGACAGCCGAGCAAGATGTGGCTTACACAGAGAGCAG 503
Oy 410 GluArgArgGArgValSerHisAspPheAlaGlnGlnArgProTyrGluAsnPhe 429
Db 502 GAAGAGAGACGAGGAGTCCCATGACCCCTTTGACAGCAAGAAGCTGAGAGATTTT 443
Oy 430 GlnAsnThrGluGlyLysGlyThrValTyrSerSerAlaAlaSerHisGlyAsnAlaVal 449
Db 442 CAGATACAGAGGAGAAAGGACAGCTGATTCAGAGTGCAGGACGATGATAGAGAGTGC 383
Oy 450 HisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyLeuTyr 469
Db 382 CACGAGCCCTCAGGCTCAGCAGCAACCTCAAGTACTGATCAGAACAAATGATTTAT 323
Oy 470 SerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAlaGlyProArgValTyr 489
Db 322 AGCTCAGCTGACTTTGGACAGAGCACTGATCCAGAGAGAGGTTCCAGAGTGG 263
Oy 490 TyrArgProLeuProSerHisMetProSerLeuHisAsnIleProValProGluThrAsn 509
Db 262 TACAGGCCAATTCACAGTCAATGCTGATATATATCCAGAGTCCGAGAGACCAAC 203

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QY      510 TyrLeuGlyAsnThrProTherMetProPheSerSerLeuProProThrAspGluSerIle 529
      |||
      202 TATCAGAGAAATACACCCACCATGCATTCACCTCTGCCACCGACAGATGATCTATA 143
DB
QY      530 LysTyrThrIleTyrAsnSerThrGlyIleGlnIleGlyAlaTyrAsnTyrMetGluIle 549
      |||
      142 AAATATACCATATACAAATGTACTGCTGATTCAGATTGCGAGCCTACAAATATATGAGATT 83
DB
QY      550 GlyGlyThrSerSerSerLeu-LeuAspSerThrAsnThrAsnProIleGlu 566
      |||
      82 GTTGGAGACAGTCTTTCACCTAGGTAGACAGACACATCTGTACATCTCGAG 31
DB
RESULT 15
LOCUS   BG387238 786 bp mRNA linear EST 12-MAR-2001
DEFINITION 602455976r1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4584235 5',
      mRNA sequence.
ACCESSION BG387238
VERSION   BG387238.1 GI:13280684
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA sequencing by: NIH Intramural Sequencing Center
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1CM1309 row: g column: 20
          High quality sequence stop: 454.
FEATURES
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             /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
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             insert size 1.8kb. Library constructed by Ling Hong in
             the laboratory of Gerald M. Rubin (University of
             California, Berkeley) using ZAP-cDNA synthesis kit
             (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 259 a 215 c 163 g 149 t
ORIGIN
Alignment Scores:
Pred. No.: 4e-84 Length: 786
Score: 864.50 Matches: 184
Percent Similarity: 80.77% Conservative: 5
Best Local Similarity: 78.63% Mismatches: 13
Query Match: 24.39% Indels: 32
DB: 12 Gaps: 6
US-09-981-397a-16 (1-671) x BG387238 (1-786)
QY      395 ThrLysGlnGlnProArg-GlnAsnValAlaTyrAsnArgGlnGluIuArgArgArg 414
      |||
      2 ACGAATACGACGCCAGTACAGAAATGTGGCTTACACAGAGAGAGAAAGAGACGCGAG 61

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QY      414 gValSerHisAspProPheAlaGlnGln-ArgProTyrGluAsnProHegInAsnThrGluG 434
      |||
      62 GGTCTCCCATGACCCCTTTTGCACACACAGACGCTTACAGAGATTTTCAGATATACAGAG 121
DB
QY      434 LylsGlyThrValTyrSerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerG 454
      |||
      122 GAAGAAGGCACTGCTTATTCACAGTCAGCCAGTCAGTAATGACATGACGACGCCCTCAG 181
DB
QY      454 LylLeuThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyP 474
      |||
      182 GGCTACACAGCCACCTCCTCAAGTACTGTATCAGAACAAATGATTTATATAGCTACATGGCT 241
DB
QY      474 HegLylThrArgProLeuAspProGlyThrAlaGlyProArgValIlePtyrArgProIleP 494
      |||
      242 TTGGAACAAGACCACTGGATTCAGAGAACAGACAGGTCGCCAGATTGGTACAGGCCAATTC 301
DB
QY      494 roSerHisMetProSerLeuHisAsnIleProValProGluThrAsnTyrLeuGlyAsnT 514
      |||
      302 CAAGTCATATGCTGCTGATGCAATATATCCAGTGCTGAGACCAACTATATAGGAATA 361
DB
QY      514 hrProThrMetProPhe-SerSerLeuProProThrAspGluSerIleLysTyrThrIle 533
      |||
      362 CACCCACCATGCCATATCAGCTCTTGGCCACACAGATGATCTATATAATATACATA 421
DB
QY      534 TyrAsnSerThrGlyIleGlnIleGlyAlaTyrAsnTyr-MetGluIleGlyGlyThrSe 553
      |||
      422 TACAAATAGTACTGGCATTCAGATCGGAGGCTTACATTTATACGAGATCGGTGGACCGA 481
DB
QY      553 rSer-SerLeuLeuAspSerThrAsnThrAsnPhe-LysGluGluProAla-AlaI 571
      |||
      482 GTCCATCCACTACTAGACCGACGACACATACGAACTTCCACAGACAGACGACGCTGCTA 541
DB
QY      571 Ys-----TyrGlnAlaIlePheAspAsnThrThrSerLeuThrAsp-LysHisL 587
      |||
      542 AGTTACCAAGTACTCTCTGATC-----AATACCACTAGTGTGACGATACCAACCAACC 595
DB
QY      587 euAspProIleArgGlnGluAsnLeuGly-----LysHisL 595
      |||
      596 TGGACCCCATCGAGCAACATGTGGGACACACCCACGCGCCACACAGGAGCCCGAANA 655
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QY      596 -----LysHisLTP 598
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      656 AATGAGGCTTCAGACACGCGCTTCAGCATTTGG 687

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Search completed: June 25, 2003, 22:29:46
Job time : 2056 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: June 25, 2003, 20:39:11 ; Search time 100 Seconds
(Without alignments)
2057.801 Million cell updates/sec

Title: US-09-981-397A-16
Perfect score: 3545
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Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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Database : Issued_Patents_NA:*

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCrus.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3545	100.0	2016	4	US-09-132-118-1
2	3545	100.0	2617	4	US-09-161-443-1
3	3529	99.5	2137	1	US-08-444-005-16
4	3505	98.9	9687	4	US-09-133-944-2
5	3505	98.9	9687	4	US-09-208-827-2
6	2423.5	68.4	2268	4	US-08-444-005-14
7	521	14.7	606	4	US-09-328-111-495
8	448	12.6	1873	3	US-09-329-418-1
9	448	12.6	1873	4	US-09-531-914-1
10	446	12.6	1557	4	US-09-329-418-2
11	446	12.6	1557	4	US-09-531-914-2
12	410.5	11.6	3516	3	US-09-188-930-257

13	375.5	10.6	1888	3	US-09-188-930-66	Sequence 66, Appl
14	371	10.5	1620	4	US-09-099-041A-3	Sequence 3, Appl
15	371	10.5	1620	4	US-09-245-281-3	Sequence 3, Appl
16	371	10.5	1620	4	US-09-207-359B-3	Sequence 3, Appl
17	371	10.5	1931	3	US-09-019-942-2	Sequence 2, Appl
18	371	10.5	1931	4	US-09-099-041A-1	Sequence 1, Appl
19	371	10.5	1931	4	US-09-245-281-1	Sequence 1, Appl
20	371	10.5	1931	4	US-09-470-271-2	Sequence 1, Appl
21	371	10.5	1931	4	US-09-207-359B-3	Sequence 1, Appl
22	371	10.5	2501	4	US-09-920-663-3	Sequence 3, Appl
23	371	10.5	2502	4	US-09-069-023-2	Sequence 2, Appl
24	354.5	10.0	4975	2	US-08-249-687C-1	Sequence 1, Appl
25	354.5	10.0	4989	2	US-08-666-392A-3	Sequence 3, Appl
26	354.5	10.0	4989	2	US-08-625-819-1	Sequence 1, Appl
27	354.5	10.0	4989	3	US-08-755-558-4	Sequence 1, Appl
28	354.5	10.0	4989	3	US-08-746-559A-1	Sequence 4, Appl
29	354.5	10.0	4989	4	US-08-880-313A-9	Sequence 1, Appl
30	354.5	10.0	4989	4	US-09-199-926-3	Sequence 9, Appl
31	354.5	10.0	4989	4	US-08-864-641B-17	Sequence 3, Appl
32	354.5	10.0	4989	4	US-09-389-855A-9	Sequence 17, Appl
33	354.5	10.0	4989	4	US-09-668-822-9	Sequence 9, Appl
34	354.5	10.0	4993	3	US-08-746-559A-3	Sequence 9, Appl
35	337.5	9.5	738	2	US-08-604-989A-8	Sequence 3, Appl
36	337.5	9.5	1398	2	US-08-604-989A-10	Sequence 8, Appl
37	337.5	9.5	1521	2	US-08-604-989A-10	Sequence 9, Appl
38	337.5	9.5	1713	4	US-09-741-154-1	Sequence 10, Appl
39	337.5	9.5	1942	2	US-08-604-989A-11	Sequence 1, Appl
40	337.5	9.5	2000	4	US-08-426-509A-1	Sequence 11, Appl
41	337.5	9.5	2000	5	PCP-US95-05008-1	Sequence 1, Appl
42	333	9.4	4149	2	US-08-737-715-1	Sequence 1, Appl
43	324.5	9.2	2443	2	US-08-685-625A-1	Sequence 1, Appl
44	319.5	9.0	1788	4	US-09-529-279-14	Sequence 14, Appl
45	319.5	9.0	2656	2	US-08-685-625A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-132-118-1
Sequence 1, Application US/09132118
Patent No. 6211337
GENERAL INFORMATION:
APPLICANT: BAICHUWAL, VIJAY R
APPLICANT: HUANG, JIANING
APPLICANT: HSU, HAILING
APPLICANT: GOEDEL, DAVID V
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/132.118
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 795-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342

:- INFORMATION FOR SEQ ID NO: 1:
:- SEQUENCE CHARACTERISTICS:
:- LENGTH: 2016 base pairs
:- TYPE: nucleic acid
:- STRANDEDNESS: double
:- TOPOLOGY: linear
:- FEATURE:
:- NAME/KEY: CDS
:- LOCATION: 1..2013
:- US-09-132-118-1

Alignment Scores:
Pred. No.: 0 Length: 2016
Score: 3545.00 Matches: 671
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4

US-09-981-397a-16 (1-671) x US-09-132-118-1 (1-2016)
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QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuCysPheHisArgThrGlnGly 40
DB 61 GCAGAACTGGACAGCGAGAGGCTTTGGAGAGTCTCTGCTTTCCACAGAACCCAGGGA 120
QY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnCysIleGluHisAsnGluAlaLeu 60
DB 121 CTCATGATCAGAAACAGTGTACAGAGGCGCCCACTCATTTGACACAGAGAGCCCTC 180
QY 61 LeuGluGluAlaLysMetLeuAsnArgLeuArgHisSerArgValValLysLeuGlnGly 80
DB 181 TTGGAGGAGCGGAAGATGATGATACAGACTGACACAGCGCGGTGTAAAGCTCTCGGCG 240
QY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
DB 241 GTCATCATAGAGAAAGGAAGTACTCCCTGGTGTATGAGTACATGAGAAAGGCACTG 300
QY 101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
DB 301 ATGCACGGCTGGAAGCGGAGATGATGATGCTCCGCTTCTGTAAAGAGGATTAATTGG 360
QY 121 GluIleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
DB 361 GAAATCATAGAGAAATGCTACTTACATGAAAAGCGGTGATACACAAAGGACCTGAG 420
QY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
DB 421 CCTGAAATATCCTGTGTTGATTAATGACTCCACATTAAGATCGCAGACCTCGGCTTGGC 480
QY 161 SerPheLysMetTrpSerLysLeuAsnAsnGluLysAsnGluLeuAlaIleValAsp 180
DB 481 TCCCTTAAGATGTGAGCAAACTGAATAATGAAAGACAAATGAGCTGAGGAGGAGTGGAC 540
QY 181 GlyThrAlaLysLysAsnGlyLysThrLeuTyrTyrMetAlaProGluHisLeuAsnAsp 200
DB 541 GGCACCCGCTTAAGAAATGGCGCACCTCTACTACATAGGCGCGCCGAGACCTTAATGAC 600
QY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValIleLeuTrpAla 220
DB 601 GTCACAGCAAAAGCCACAGAGAACTCGGATGTATACAGCTTGGCTGTAGTACTCTGGGCG 660
QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCys 240
DB 661 ATATTTCAAATAAGAGACCATATGAAATGCTATCTGTGAGCAGACGATTGATATGTCG 720
QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
DB 721 ATAAATCTGGGAAGCGCCAGATGTGATCATCTAGTACTGCGCCAAAGAAAT 780

QY 261 IleSerLeuMetLysLeuCysTrpGluAlaAsnProGluAlaArgProThrPheProGly 280
DB 781 ATCACTCATAGAGCTCTGCTGGGAACGGAATCCGGAAGCTCGGCCACATTTCTGCGC 840
QY 281 IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAsp 300
DB 841 ATTGAAGCAAAATTTAGAGCTTTTATTATTAATCAATTAAGAAAGAGTGTAGAGAGCAG 900
QY 301 ValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValValLysArgMetGlnSer 320
DB 901 GTGAAGATTTAAAGAAAGAGTATTCAACAAAATGCAATGTGAAAGCAATCAGTCT 960
QY 321 LeuGluLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
DB 961 CTTCACTGATTGTGTGCGAGTACTTCAAGCCGCTTAATTTACCCACAGAACAGCTCT 1020
QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAla 360
DB 1021 GGTTCACCTGCACAGTCCCGAGGACTTGGATGGGTCTGTGGAGAGTCTGGTTGCT 1080
QY 361 ProSerLeuGluHisProGlnGluLysAsnGluProSerLeuGlnSerLysLeuGlnAsp 380
DB 1081 CTTTCCCTGGAGCACCCCAAGAGAGATGAGCCCACTGCGAGATTAACCTCCAGAGC 1140
QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
DB 1141 GAAGCCAACTACCATCTTTATGCGACGCGCATGACAGCGAGAGCAAGAAACAGACCCAGA 1200
QY 401 GlnAsnValAlaTyrAsnArgGluGluGluLysArgArgValSerHisAspProPhe 420
DB 1201 CAGAAATGGCTTACACAG 1260
QY 421 AlaGlnGlnArgProTyrGluAsnPheGluAsnThrGluGlyLysGlyThrValTyrSer 440
DB 1261 GCACAGCAAGACCTTTACAGAGATTTTCAGATACAGAGGAGAAAGGCATCTGTATTCC 1320
QY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
DB 1321 AGTCGAGCAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 461 ValLeuTyrGluAsnAsnGlyLeuTyrSerHisGlyPheGlyThrArgProLeuAsp 480
DB 1381 GTACTGTATCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 481 ProGlyThrAlaGlyProArgValTrpTyrArgProIleProSerHisMetProSerLeu 500
DB 1441 CCAGGAACAGAGTCCAGAGTTGGTACAGGCCAATTCCAAGTCAATATGCTTAATGCTG 1500
QY 501 HisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSer 520
DB 1501 CATATATTCACAGGCTCGAGACCAACATATAGGAATACACCACCATGCCATTGACG 1560
QY 521 SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
DB 1561 TCCCTGGCACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 541 IleGlyAlaTyrAsnTyrMetGluIleGlyLysHisSerSerLeuLeuAspSerThr 560
DB 1621 ATTGAGACCTTAATTAATGAGATGAGTGGAGGAGGATTCATCATAGAGAGAGCA 1680
QY 561 AsnThrAsnPheLysGluGluProAlaAlaLysTyrIleAlaIlePheAspAsnThrThr 580
DB 1681 AATACGAACCTCAAG 1740
QY 581 SerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTrpLysAsn 600
DB 1741 AGTCTGACGAGTAAACACTGAGCCCAATGAGGAAATCTGGGAAAGCACTGGAAGAAC 1800
QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGlu 620
DB 1801 TGTGCCCCGTAAACGGGCTTTCACACAGTCTCAGATTGATGAATAATGACCATGATAGAG 1860

Oy	621	Argaspqjleuylsglylsvaltyrlyglmetleuglnlystprvalmetarglucly	640
Db	1861	CGAATGACTGGAAGAAAGAGTTTACCAGATGCTCCAAAAGTGGTGATGAGGAAGC	1920
Oy	641	llylsglylathrvalrglylsleuAlaglnAlaleuHlsglnCysSerArgIleasp	660
Db	1921	ATTAAGGAGGAGCCAGGTGGGGAAGCTGGGCCAGGCGCTCCACAGTGTTCAGGATGCAC	1980
Oy	661	leuLeuSerSerleulleltyrvalserGlnAsn	671
Db	1981	CTTCTGAGCAGCTTGATTTAGCTACGCCAGAAC	2013

RESULT 2
US-09-161-443-1
: Sequence 1, Application US/09161443A
: Patent No. 6020198
: GENERAL INFORMATION:
: APPLICANT: C. Frank Bennett
: APPLICANT: Lex M. Cowsett
: TITLE OF INVENTION: ANTISENSE MODULATION OF RIP-1 EXPRESSION
: FILE REFERENCE: RTS-001
: CURRENT APPLICATION NUMBER: US/09/161.443A
: CURRENT FILING DATE: 1998-09-25
: NUMBER OF SEQ ID NOS: 47
: SEQ ID NO 1
: LENGTH: 2617
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(2016)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 2141
: OTHER INFORMATION: unknown
: FEATURE:
: NAME/KEY: unsure
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: OTHER INFORMATION: unknown
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 2496
: OTHER INFORMATION: unknown
US-09-161-443-1

Alignment Scores:
Pred. No.: 0 Length: 2617
Score: 3545.00 Matches: 671
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 3

US-09-981-397A-16 (1-671) x US-09-161-443-1 (1-2617)

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Oy	21	AlaGluleuAspSerGlyGlyPheGlyLysValserLeuCySPheHlsArgThrGlnGly	40
Db	61	GCAGAACTGGCAGACGGAGCGTTTGGGAGAGTGCTCTGTGTTCACAGAACCCAGGGA	120
Oy	41	LeuMetIleMetLysThrValTyrLysGlyProAsnCysIleGlnHlsAsnGlnAlaLeu	60
Db	121	CTCATGTATCATGAAACAGTGTACAAAGGGCCCCAACATGACATTGAGCAACAGAGCCCTC	180
Oy	61	LeuIleGlnAlaLysMetMetAsnArgLeuArgHlsSerArgValValLysLeuLeuGly	80

Dd	181	ITGCAAGGAGCGCAAGATCATATCAACAGATGAGACACAGCCGGGTGGTGAACCTCTGGCC	240
Qy	81	VallIleIleIleGluGluGlyLysTyrSerLeuValMetGlyIrrMetGluLysGlyAsnLeu	100
Dd	241	GTCATCATATAGAGAGAGGAACTACTCCCTGGTGTGGATGCTACATGAGAAAGCCACCTG	300
Qy	101	MethIsvaLleuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu	120
Dd	301	ATGCACGGCTGAAAGCCGAGATAGATCTCCGCTTCTGTAAAGAGAAAGATATTTTG	360
Qy	121	GluIleIleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys	140
Dd	361	GAATCATATTGAGAGAAATGCTCTACTTACATGAAAGAGCGTGAATACACAGAGCTTAGAG	420
Qy	141	ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla	160
Dd	421	CCTGAATAATCTCTTGATTAATAGACTCTCCACTTAAGATCGCAGACTCGGCTTGCC	480
Qy	161	SerPheLysMetTrpSerLysLeuAsnAsnGluLysAsnGluLeuArgGluValAsp	180
Dd	481	TCCTTTAAGATGTGAGCAACCTGAATATGAAAGACAAATGAGCTGAGAGGAAGTGGAC	540
Qy	181	GlyThrAlaLysLysAsnGlyGlyThrLeuLysTyrMetAlaProGluHisLeuAsnAsp	200
Dd	541	GGCACCGCTAGAAAGAAATGGCGGACCTCTACTACATGAGCGCCGAGCACTTAATGAC	600
Qy	201	ValAsnAlaLysProThrGluLysSerAspAlaIrrSerPheAlaValIleuTrpAla	220
Dd	601	GTCACAGCAAAAGCCCAACAGACACTCGGATGTGTACACGCTTGGTGTATGACTCTGGGCG	660
Qy	221	IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGluLeuIleMetCys	240
Dd	661	ATATTGCAATTAAGAGACCATATGAAATCTATCTGTGAGCAGCACTTGAATATGTGC	720
Qy	241	IleLysSerGlyAsnArgProAspValAspAspIleThrGlyTyrCysProArgGluIle	260
Dd	721	ATAAATCTGTGGAAACAGCCAGATGTGATGATCACTCATGTGACTGTGCCCAAGGAATTT	780
Qy	261	IleSerLeuMetLysLysLeuCysTrpGluAlaAsnProGluAlaArgProThrPheProGly	280
Dd	781	ATCAGTCTCATGAAAGCTCTGCTGGGAACCGAATCCGGAAGCTGGCGGACATTTCCGTGGC	840
Qy	281	IleGluGluLysPheArgProPheTyrLeuSerGluLeuGluGluSerValGluLysP	300
Dd	841	ATTGAGCAAAATTTAGSCCTTTTATTATTAGTCAATTAGCAAGAAAGTGTCAGAGAGAC	900
Qy	301	ValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValValLysArgMetGlnSer	320
Dd	901	GTGAAGATTTTAAAGAAAGACTATTTCAACAAATGCAAGTTGGAAGAGAGATCAAGTCT	960
Qy	321	LeuGluLeuAspCysValAlaIleValProSerSerArgSerAsnSerAlaThrGluGlnPro	340
Dd	961	CTTCACACTGGAATGTGTGGACAGTACTTCAAGCCGGTCAATTTAGCCACAGAACAGCTT	1020
Qy	341	GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAla	360
Dd	1021	GGTTCACAGCAGACTTCCACAGGACTTGGATGGTGGTCTGTGGAGAGAGTCTGCTTGGCT	1080
Qy	361	ProSerLeuGluHisIrrProGluGluLysAsnGluProSerLeuGlnSerLysLeuGlnAsp	380
Dd	1081	CTTCTCCCTGGAGACCCACAGAAAGAGATGATGAGCCCAAGCTCGCAGAGATTAACCTCAAGAC	1140
Qy	381	GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg	400
Dd	1141	GAAGCCAACTACCATCTTTATGGCAGCCGCTGGACAGCCAGACGAGCAACAGACGCCACAGA	1200
Qy	401	GlnAsnValAlaTyrAsnArgGluGluGluValArgIrrArgArgValSerHisAspProPhe	420
Dd	1201	CAGATATGGCTTTCAACACAGAGAGAGAAAGAGAGCAGCAGGCTCTCCATGACCTTTT	1260
Qy	421	AlaGlnGlnAlaArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSer	440
Dd	1261	GCACAGCAAAACCTTTACAGAAATTTTTCAGATATCAAGAGGAAAAAGCCACTGTTTATTTCC	1320

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OY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
DB 1321 AGTCAGCGCAGTCAGTATATGATGCAATGCACCGCCCTCAGGCTCACCAGCCAACTCTCA 1380
OY 461 ValLeuTyrglnAsnAsnGlyLeuTygSerSerHisGlyPheGlyThrArgProLeuAsp 480
DB 1381 GTACTGTATCAGAACAAATGATATATAGCTCACAATGCTTGTGGAAACAGCACTGGAT 1440
OY 481 ProGlyThrAlaGlyProArgValTrpIlyArgProIleProSerHisMetProSerLeu 500
DB 1441 CCAGAACACGACGATCCCAAGATTGGTACAGGCCCAATCCAGTCATATGCTATGTCG 1500
OY 501 HisAsnIleProValProGluThrAsnTygLeuGlyAsnThrProThrMetProPheSer 520
DB 1501 CATATATCCAGTCTCTGAGACCAATATCTAGAAATATACCCACCATGTCATTCAGC 1560
OY 521 SerLeuProProThrAspGluSerIleIyStryThrIleTygAsnSerThrGlyIleGln 540
DB 1561 TCCTTGGCCACCAACAGATGAATCTATAAATATACCAATATCAATAGTACTGGCATTCAG 1620
OY 541 IleGlyAlaTygAsnTygMetGluIleGlyGlyThrSerSerLeuLeuAspSerThr 560
DB 1621 ATTGACAGCTCAATATATATGAGATGTGGAGAGCTCTCACTACTACACAGCACA 1680
OY 561 AsnThrAsnPheTygGluProAlaAlaTygTygAlaIlePheAspAsnThrThr 580
DB 1681 AATACGAACTTCAAAAGAGACCCAGCTGCTAGTACCAAGCATCTTTGATATATCCACT 1740
OY 581 SerLeuThrAspIlyHisLeuAspProIleArgGluAsnLeuGlyLysHisTyrPlyAsn 600
DB 1741 AGTCAGCGATAAACACCTGAGCCCAATCAAGGAAATCTGGGAAACACACGGAAGAAAC 1800
OY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGln 620
DB 1801 TGTGCCCTTAACCTGGCTTACACAGCTCAGATTCATGAATTCACCATGACTATATAG 1860
OY 621 ArgAspGlyLeuLysGlyLysValTygIleMetLeuGlnLysTyrValMetArgGly 640
DB 1861 CGAGATGAGCTGAAGAAAGATTACAGATGCTCCAAAGTGGGTGATGGGGAAGGC 1920
OY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgTyrLeu 660
DB 1921 ATAAAGGAGCCAGCGTGGGGAAGCTGGCCAGCGCTCCACACAGTCTCCAGATCGAC 1980
OY 661 LeuLeuSerSerLeuIleTygValSerGlnAsn 671
DB 1981 CTTCTGAGCAGCTTGATTTAGCTACGCCAGAAC 2013

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RESULT 3

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US-08-444-005-16
: Sequence 16, Application US/08444005
: Patent No. 5674734
: GENERAL INFORMATION:
: APPLICANT: Leder, Philip
: APPLICANT: Seed, Brian
: APPLICANT: Stanger, Ben Z.
: APPLICANT: Lee, Tae-Ho
: APPLICANT: Kim, Emily
: TITLE OF INVENTION: CELL DEATH PROTEIN
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street, Suite 3100
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/444,005
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,164
: REFERENCE/DOCKET NUMBER: 00383/026001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2137 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
US-08-444-005-16

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Alignment Scores:
Pred. No.: 0 Length: 2137
Score: 3529.00 Matches: 668
Percent Similarity: 99.70% Conservative: 1
Best Local Similarity: 99.55% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 1 Gaps: 0

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US-09-981-397A-16 (1-671) x US-08-444-005-16 (1-2137)

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DB 1 ATGCACACAGACATTCCTTGAATGTCAATTAAGATGAATCCAGAGACTTCTTGAGAGCT 60
OY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuCysPheHisArgThrGlnGly 40
DB 61 GCAGAACTGACGACGCGGAGGCTTCGGGAAGCTGTCTGTGTTCCACAGAACCCAGGAGA 120
OY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnGlyIleGlnHisAsnGluAlaLeu 60
DB 121 CTCATGATCATGAAGAAAGCTGTACAAAGGGCCCACTGCATTTGAGACACAGAGCCCTC 180
OY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValIValLysLeuLeuGly 80
DB 181 TTGAGAGAGCGGAAGATGATGACAGACTGAGACACACCCGGTGGTAACTCTGGGC 240
OY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
DB 241 GTCATCATGAGAGGAGGAGAGTACTCCCTGGTGTGATGAGCATGACATGCAAGGCAACCTG 300
OY 101 MethisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
DB 301 ATGCACGTGCTGAAGCCGAGATGATGACTCCGCTTCTGTGTAAGGAAGGATTAATTTTG 360
OY 121 GluIleIleGluGluMetCysTyrLeuHisGlyValIleHisLysAspLeuLys 140
DB 361 GAAATCATTTGAAGGATGCTGCTACTTACATGGAAGGCGATACACAAAGACTGAG 420
OY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
DB 421 CCTGAAATATCTCTTGTGATATGACTTCCACATTAAGATGCGACGACCTCGGCTTGGC 480
OY 161 SerPheLysMetTyrPserLysLeuAsnAsnGluGlnHisAsnGluLeuArgGluValAsp 180
DB 481 TCCTTTAAGATGTGAGCAAACTGAATATATGAAGGACCAATGAGCTGAGGGAAGTGGAC 540
OY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAsp 200
DB 541 GGCAACGCTAGAGAAATGGCGGACCTCTACTACATAGGCGCCGAGACACTGAAATGAC 600
OY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValIleLeuTyrPala 220

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Db      601  GTCAAGCAAGCCACAGAGAGAGTGGAGTGTACAGCTTTGCTGTAGTACTCTGGCG 660
Qy      221  ILepheAAsenLysGluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCys 240
Db      661  ATATTGGCAATATAGAGAGCCATATGAAATGCTATCTGTGACGACGACATTTATATGTC 720
Qy      241  ILelySerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
Db      721  ATAAATCTGGGAGACAGCCAGATGTGGATGACATCATGTGACTGAGTCCCAAGAAATT 780
Qy      261  ILeserLeuMetLysLeuGlyTyrGluAlaAsnProGluAlaArgProThrPheProGly 280
Db      781  ATCAAGTCTCATGAAGCTCTGCTGGGAAGCCGAATCCGGAAGCTCGCCACATTTCTGGC 840
Qy      281  ILleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluLysSerValGluLysAsp 300
Db      841  ATTGAAGAAAATTAGGCTTTTATTTATTTAGTCATTTAGAGAAAGAGTGAAGAGAGAC 900
Qy      301  VallysSerLeuLysLysGluTyrSerAsnGluAsnAlaValLysArgMetGlnSer 320
Db      901  GTGAAGAGTTTAAAGAAAGAGTATTCAAACGAAATGCGAGTTGTGAAGAGAAATGCGACT 960
Qy      321  LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluLysPro 340
Db      961  CTTCAACTGATTTGTGGCAGTACCTTCAAGCGGTCAAATTCAGCCACAGAACAGGCT 1020
Qy      341  GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGlnSerTyrPheAla 360
Db      1021  GGTTCACCTGCACATTTCCACAGGACTTGGATGGGTCTGTGGAGAGACTCTGTGTTGGT 1080
Qy      361  ProSerLeuGlnHisProGlnGluAsnGlnProSerLeuGlnSerLysLeuGlnAsp 380
Db      1081  CCTTCCTCGAGCACCACAGAGAGAGATGAGCCACCTCGCAGAGTAAACTCCAAAC 1140
Qy      381  GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
Db      1141  GAAGCCCAACTACCTCTTATGTGACCGCGGTGACAGGACAGGAAACACACCCACGA 1200
Qy      401  GlnAsnValAlaTyrAsnArgGluGluLysArgArgValSerHisAspProPhe 420
Db      1201  CAGAAATGGCTTTCACACAGAGAGAGAGAAAGAGAGCGGCTCTCCATGACCTTTT 1260
Qy      421  AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluLysGlyThrValTyrSer 440
Db      1261  GCACAGCAAGAGCCTTACGAGAAATTTTCAGAAATACAGAGGAGGACATTTATTC 1320
Qy      441  SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
Db      1321  AGTCACCCAGCTCATGTGAATGAGTGCACACAGCCATCAGGGCTCACCCAGCAACTCA 1380
Qy      461  ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
Db      1381  GTACTGTATCGAACATGATGATTTATATGCTCACAATGGCTTTGGAAACAGCCACTGGAT 1440
Qy      481  ProGlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeu 500
Db      1441  CCAGAGAACAGAGCTCCAGAGTTTGGTACAGGCCAATTCACAGTCATATCCATGCTG 1500
Qy      501  HisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSer 520
Db      1501  CATATATATCCAGAGCTCGAGACCACTATCTAGGAAATTTCTCCACCATCCATTCAGC 1560
Qy      521  SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
Db      1561  TCCCTGGCACCAAGATGATCTATATAATATATACCATATACATATAGACTGGCACTTCA 1620
Qy      541  ILleGlyAlaTyrAsnTyrMetGluIleGlyLysThrSerSerSerLeuLeuAspSerThr 560
Db      1621  ATTGAGACCTTACATATATATGATGATGTGGGACGAGTTTCATCAGTACTAGACAGACA 1680
Qy      561  AsnThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
Db      1681  AATACGAACCTTCAAGAGAGAGCCAGCTGCTAAGTACCAAGCTATCTTGATATATACACT 1740

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Qy      581  SerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTyrLysAsn 600
Db      1741  AGTCGACGAGTAAACACCTGACCCATTCAGGAAATCTGGCAACACCTCGCAAAAC 1800
Qy      601  CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGlu 620
Db      1801  TGTGCCCTTAACCTGGCGCTTCACACAGCTCAGATGTGAATTCAGACATGACTATGAG 1860
Qy      621  ArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTyrPValMetArgGluGly 640
Db      1861  CGAGATGGACCTGAAAGAAAGATTATACAGATGCTCCAAAAGTGGGTATGAGGAAGGC 1920
Qy      641  ILelysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
Db      1921  ATAAAGAGGACGACGCTGGGAGAGCTGGCCACAGCGCTCCACAGCTGTCCAGATGAGAC 1980
Qy      661  LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
Db      1981  CTTCTGACGACCTTGATTTACGTCAGCCAGAAC 2013

RESULT 4
US-09-133-944-2
: Sequence 2, Application US/09133944
: Patent No. 6280937
: GENERAL INFORMATION:
: APPLICANT: Luo, Ying
: APPLICANT: Yu, Pei Wen
: APPLICANT: Lorens, James
: TITLE OF INVENTION: SHUTTLE VECTORS
: FILE REFERENCE: A66252/DJB/DAV
: CURRENT APPLICATION NUMBER: US/09/133, 944
: CURRENT FILING DATE: 1999-08-14
: EARLIER APPLICATION NUMBER: 09/133, 949
: EARLIER FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 9687
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: constructed
: OTHER INFORMATION: vectors
US-09-133-944-2

Alignment Scores:
Pred. No.: 0 Length: 9687
Score: 3505.00 Matches: 668
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 2
Query Match: 98.87% Indels: 1
DB: 4 Gaps: 0

US-09-981-397A-16 (1-671) x US-09-133-944-2 (1-9687)
Qy      2  GlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSerAla 21
Db      1134  CACCCAGACATGCTCTTGAATGTCATTAAGTGAATTCACATGACTTCTGGAAGTGA 1193
Qy      22  GluLeuAspSerGlyGlyPheGlyLysValSerLeuCysPheHisArgThrGlnGlyLeu 41
Db      1194  GAACTGACACCGAGAGGCTTTGGGAAGGTGCTGTGTCTTCCACAGAACCCAGAGACTC 1253
Qy      42  MetIleMetLysThrValTyrLysGlyProAsnCysIleGluHisAsnGluAlaLeuLeu 61
Db      1254  ATGATTCATGAAGAAAGTGTACAGGGGCCCAACTGCATGTAGACACAGAGAGCCCTTG 1313
Qy      62  GlnGluAlaLysMetMetAsnArgLeuArgHisSerArgValAlaLysLeuLeuGlyAla 81
Db      1314  GAGGAGGGGAGATGATGAACAGACTGAGACACAGCGGGGTGGTGAAGCTTCTGGCGCTC 1373
Qy      82  IleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMet 101

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Db      1374 ATCATAGAGGAGGAGACTCCCTGGATGAGTACATGAGAGGCAACCTGATG 1433
Oy      102 HisValLeuValAlaGluMetSerThrProLeuSerValLysGlyArgIleLeuGlu 121
Db      1434 CAGGTCGTAAGAGCCGAGTAGTACTCCGCTTCTGTAAAGAGGTAATTTGGGAA 1493
Oy      122 IleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysPro 141
Db      1494 ATCATTTGAAGAAATGTGCTACTTACATGA - AAGAGCTGATACACAGAGCACTGAAGCTT 1552
Oy      142 GluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSer 161
Db      1553 GAAATATCTCTTGTGATATGACTTCCACATTAGATCGCAGACCTCGGCTTCCCTCC 1612
Oy      162 PheLysMetTyrPheSerLysLeuAsnAsnGluGluHisAsnGluLeuArgLysValAspGly 181
Db      1613 TTTTAGATGTGGAGCAAACTGATATGAGAGCAAAATGAGCTGAGGAACTGAGCGGC 1672
Oy      182 ThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspVal 201
Db      1673 ACCGCTAGAAGAAATGGGGGACCCCTACTATCATGGCGCCGAGCACCCTGATGACGTC 1732
Oy      202 AsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuTyrPalaIle 221
Db      1733 AACGCAAGCCCAAGAGAGAGCGATGTGTACAGCTTGTCTGTAGTACTGTGGCGCAT 1792
Oy      222 PheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGluLeuIleMetCysIle 241
Db      1793 TTTGCAATTAAGAGCACTATGAAATGCTATCTGTGAGCAGCACTTGAATATGTGCATA 1852
Oy      242 LysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgIleIleIle 261
Db      1853 AAATCTGGGACAGAGCCAGCATGTGATGATGATCATCATGATGATGCCCAAGAAATTTTC 1912
Oy      262 SerLeuMetLysLeuCysTyrGluAlaAsnProGluAlaArgProThrPheProGlyIle 281
Db      1913 AGTCTCAAGAAAGCTCTGTGTGGAAAGCGAATCGGAAAGCTCGGCCACATTTCTGTGCAT 1972
Oy      282 GluGluLysPheArgProPheTyrLeuSerGlnLeuGluLysValGluGluLysAspVal 301
Db      1973 GAAGAAATTTAGGCTTTTATTTATTTAGTCAATTAGAAAGAGGTGTGAAGAGAGACGTG 2032
Oy      302 LysSerLeuLysLysGlyTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeu 321
Db      2033 AAGAGTTTAAAGAAAGATATTCAAAACGAAATCGAGTTGGAAGAGATGACAGTCTCTT 2092
Oy      322 GlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnProGly 341
Db      2093 CAACCTGATGTGTGGCAGTACTCTTCAAGCCGCTCAAAATTCAGCCACAGAACAGCCTGT 2152
Oy      342 SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTyrPheAlaPro 361
Db      2153 TCACGTGCACAGTCCACAGGAGCTTGAGTGGTCTCTGTGGAGAGATCCTGTGTTCTCTCT 2212
Oy      362 SerLeuGlnHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAspGlu 381
Db      2213 TCCTGTGGAGCACCCACAGAGAGATGAGCCACGCTCGAGAGTAACCTCCACAGACGAA 2272
Oy      382 AlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGln 401
Db      2273 GCCAAGTACCAATCTTTATGTGACCGCGCATGAGCAGCAGCAACACACACCCGAGAG 2332
Oy      402 AsnValAlaTyrAsnArgGluGluLysArgArgArgValSerHisAspProPheAla 421
Db      2333 AATGTGGCTTACACACAGAGAGAGAGAAAGACGACGAGGTCTCCCATGACCTTTTCCA 2392
Oy      422 GlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSerSer 441
Db      2393 CAGCAAGAGCCCTTACAGAAATTTTCAGATACAGAGGAGGAAAGGACACTGTTATTCAGT 2452
Oy      442 AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnVal 461

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Db      2453 GCAGCCAGTATGATTAATGATGATGACAGCCAGCCCTCAGGAGCTCACCAGCCAACTCAAGTA 2512
Oy      462 LeuTyrGlnAsnAsnGlyLeuTyrSerHisGlyPheGlyThrArgProLeuAspPro 481
Db      2513 CTGTATCAAGAAATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 2572
Oy      482 GlyThrAlaGlyProArgValTyrPtyArgProIleProSerHisMetProSerLeuHis 501
Db      2573 GGAACAGCAGCTCCAGAGATTTGTGTACAGGCCAATTTCCAGTCATATGCTGTGAT 2632
Oy      502 AsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSer 521
Db      2633 AATATCCAGTACCTGAGACCACTATCTAGAAATATACCCACCATGCTGATGACGCTCC 2692
Oy      522 LeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGlnIle 541
Db      2693 TTGCCACCAACAGATGATCTTAAATAATATACATATCAATATGATGATGATGATGATGAT 2752
Oy      542 GlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerLeuLeuAspSerThrAsn 561
Db      2753 GGAGCTTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2812
Oy      562 ThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSer 581
Db      2813 ACGAATTCCAAGAGAGAGACCACTGCTTAAATGATGATGATGATGATGATGATGATGATGAT 2872
Oy      582 LeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTyrLysAsnCys 601
Db      2873 CTGACGATTAACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2932
Oy      602 AlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGluArg 621
Db      2933 GCCCTTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2992
Oy      622 AspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTyrPalaMetArgGluGlyIle 641
Db      2993 GATGACCTGAAGAAAGATTTTACAGATGCTCCAAAGTGGTGTATGAGGAGAGCAT 3052
Oy      642 LysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAspLeu 661
Db      3053 AAGGAGCCACGCTGGGAGAGCTGGCCCAAGCGCTCCACAGTGTTCAGGATGACCTT 3112
Oy      662 LeuSerSerLeuIleTyrValSerGlnAsn 671
Db      3113 CTGACGACCTGATTTAGCTCAGCCAGAAC 3142

RESULT 5
US-09-208-827-2
; Sequence 2, Application US/09208827
; Patent No. 6391582
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHOT/LE VECTORS
; FILE REFERENCE: A66252-1/DJB/DAV
; CURRENT APPLICATION NUMBER: US/09/208,827
; CURRENT FILING DATE: 1998-12-09
; EARLIER APPLICATION NUMBER: 09/133,949
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9687
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: constructed
US-09-208-827-2
Alignment Scores: 0 Length: 9687
Pred. No.:

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Score: 3505.00 Matches: 668
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 2
Query Match: 98.87% Indels: 1
DB: 4 Gaps: 0

US-09-981-397a-16 (1-671) x US-09-208-827-2 (1-9687)

QY 2 GluProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGluSerAla 21
DB 1134 CAACGACACATGCTCTGAAATGATCATTAAGATGAATCACTGACTCTCTGAGAGTGC 1193
QY 22 GluLeuAspSerGlyGlyPheGlyLysValSerLeuGlySerPheHisArgThrGlnGlyLeu 41
DB 1194 GAACTGGACAGCGGAGGCTTTGGAGAGTCTCTGTTGTTCCACAGAACCCAGGAGACTC 1253
QY 42 MetIleMetLysThrValTyrLysGlyProAsnCysIleGlnHisAsnGluAlaLeuLeu 61
DB 1254 ATGATCTCATGAAGACAGTGTACAGGGGCCCACTGCTATGACACAGAGGCGCTCTTG 1313
QY 62 GluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuGluGlyAla 81
DB 1314 GAGAGGCGGAGAGATGATGACAGACAGACAGCGGGGTGGTGAAGCTCTGGGGCTC 1373
QY 82 IleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMet 101
DB 1374 ATCATATGAGAGAGGAGGAGTACTCCCTGCTGATGAGATACATGAGAAAGGCAACCTGATG 1433
QY 102 HisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeuGlu 121
DB 1434 CACCTGCTGAAGCGAGATGAGTACTCCCTTCTGTAAAGAGAGATTAATTTGGGAA 1493
QY 122 IleIleGluGluMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysPro 141
DB 1494 ATCATGTAAGAGAAATGCTCTACTACTACATGA-AAAGCGGTGATACACAGAGACTGAAGCT 1552
QY 142 GluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSer 161
DB 1553 GAAATATTCCTTCTGTGATTAATGACTTCCACATTAAGATCCGACAGCTCGGGCTTCCCTCC 1612
QY 162 PheLysMetThrProSerLysLeuAsnAsnGluGlnHisAsnGluLeuAsnArgGluValAspGly 181
DB 1613 TTATAGATGTGGACCAACTGAATTAATGAAGACACATGAGCTGAGGAGGAGTGGAGGCT 1672
QY 182 ThrAlaLysLysAsnGlyLysThrLeuTyrTyrMetAlaProGluHisLysAsnAspVal 201
DB 1673 ACCGCTAAGAGATGGCGGACCTCTACTACTAGGCGCGCGGACACTGAATGACGCTC 1732
QY 202 AsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuTrpAlaIle 221
DB 1733 AAGCGAAAGCCCAAGAGAGTGGATGCTGATACAGCTTTGCTGTAGTACTCTGGGCGATA 1792
QY 222 PheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCysIle 241
DB 1793 TTATGCAATTAAGGAGCCATTAAGAAATGCTATCTGTAGACGAGCTGATTAATGTGATA 1852
QY 242 LysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIleIle 261
DB 1853 AAATCTGGGAAGCGCAGATGTGATGACATCTCTGATGACTCTCCCAAGAGAAATTAATC 1912
QY 262 SerLeuMetLysLeuGlyTyrGluAlaAsnProGluAlaArgProThrPheProGlyIle 281
DB 1913 AGTCTCATGAAGCTCTGCTGGAGAGCAATCCGAGACCTGGCGGACATTTCCGCGCAT 1972
QY 282 GluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspVal 301
DB 1973 GAAGAAAAAATTTAGCCCTTTTATTTAATTAAGCAATTAAGAAAGTGAAGAGAGAGAGCTG 2032
QY 302 LysSerLeuLysLysGlyTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeu 321
DB 2033 AAGAGTTTAAAGAAAGAGTATTCAAAGAAATCTCAGTTGTGAAGAGAAATGCACTCTCT 2092
QY 322 GlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnGlnProGly 341

DB 2093 CAACCTTGATTTGTGGAGTACCTTCAAGCGCGGTCAAAATTCAGCCACAGAACACCTGTG 2152
QY 342 SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaPro 361
DB 2153 TCACCTGCACACTTCCACAGGACCTTGGATGGGTCTCTGGAGAGAGCTCTGTTGCTCTCT 2212
QY 362 SerLeuGlnHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAspGlu 381
DB 2213 TCCCTGGAGACCCACAAAGAGAGATGAGCCGCGTGCAGAGTAAATCTCAAGACGAA 2272
QY 382 AlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGln 401
DB 2273 GCCAAGTACCACTTATTTATGCGACCGCATGAGACAGGAGAGAGAAACAGCACCCACAGAC 2332
QY 402 AsnValAlaTyrAsnAspGluGluGluValArgArgArgValSerHisAspProPheAla 421
DB 2333 AATGTGCTTACACAG 2392
QY 422 GlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSerSer 441
DB 2393 CAGCAAGACCTTACAGAGAAATTTTACAGATACAGAGGAAAGGACACTGTTATTTCCAGT 2452
QY 442 AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnVal 461
DB 2453 GCAGCCAGTCACTGTGATATGACAGTGCACACAGCCCTCAGGCGCTCACACAGCAACTCAAGTA 2512
QY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
DB 2513 CTGATACAGAACATGATTAATTAATGCTACATGCTTTGGAAACAGCCACTGATTCGA 2572
QY 482 GlyThrAlaGlyProAspValTyrPyrArgProIleProSerHisMetProSerLeuHis 501
DB 2573 GGAACAGAGGCTCCACAGAGTTTGTGTACAGGCAATTCGAATCATATGCCATGCTGCAT 2632
QY 502 AsnIleProValProGluThrAsnTyrLeuGlnLysAsnThrProThrMetProPheSerSer 521
DB 2633 AATATCCAGAGCTGAGACCACTATAGGAATACACCCACCATGCCATTCAGCTCC 2692
QY 522 LeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGlnIle 541
DB 2693 TTGGCCACCAACAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2752
QY 542 GlyAlaTyrAsnTyrMetGluIleGlyLysThrSerSerSerLeuLeuAspSerThrAsn 561
DB 2753 GGAGCCCTACATTTATATGAGAAATGTGTGGAGAGAGTATCATCTACTAGACAGCAACAAT 2812
QY 562 ThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSer 581
DB 2813 ACGAACTTCAAG 2872
QY 582 LeuThrAspLysHisLysLeuAspProIleArgGluAsnLeuGlyLysHisTrpLysAsnGly 601
DB 2873 CTGACGAGATTAACACCTGGAGCCCAATCAGGAAATCTGGGAAAGCACTGGAAAGAACTCT 2932
QY 602 AlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGluArg 621
DB 2933 GCCCGTAAACCTGGGCTTCACACAGTCTCAGATTATGAATTAATGACCATGACTATGAGCGA 2992
QY 622 AspGlyLeuLysGluLysValTyrGlnMetLeuGlnHisTrpValMetArgGluGlyIle 641
DB 2993 GATGAGACTGAAGAAAGGTTTACAGATGTCTCAAAAGTGGTGATGAGAGAGAGAGAGATA 3052
QY 642 LysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAspLeu 661
DB 3053 AAGGAGCCACAGGAGGAG 3112
QY 662 LeuSerSerLeuIleTyrValSerGlnAsn 671
DB 3113 CTGAGCAGCTTGATTTTACGTACAGCCAGAAC 3142
RESULT 6
US-08-444-005-14

Db	1423	-----ACAGTTGGACCAATGGAATGTGATATATACAGATGATT-----	1461
Oy	480	AspProGlyThrAlaGlyProAlrValTrpTyrAlaGProIleProSerHisMetProSer	499
Db	1462	-----GGAACTACAGGTACAGAGAGTTGGTATCCGCCAAATCTAAGCAATGATAGT	1515
Oy	500	LeuHisAsnIleProValProGluThrAsnTyrIleuGlyAsnThrProthMetProPhe	519
Db	1516	ACTTATTAATAACTCCAGATCCGAGAACCACAACTACCCGGAACACACCACCATCCCATAC	1575
Oy	520	SerSerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThGlyLe	539
Db	1576	TTTCCTGGCCGAGTACAGATGACGATCCTCATATAATATATCTATATTCATATAGTTCGGTAT	1635
Oy	540	GlnIleGlyAlaTyrAsnTyrMetClnIleGlyGlyThrSerSerSerLeuAspSer	559
Db	1636	CAGATTGGAAACCAACAAATTATATGATGATGGTTCGATGCAATTCAC-----CAACCA	1683
Oy	560	ThrAsnThrAsnPhelysGluGluProAlaAlaLysTyrGlnAlaAlaIlePheAspAsnThr	579
Db	1684	CCAAACCAATACCTGCTCAAGAGAGTGCAGCTCCAGACACCAAGGCACTCTTGATTAACACC	1743
Oy	580	ThrSerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTyrLys	599
Db	1744	ACTAGTGTGACTGATGAACACCTTAACCTTCTACAGGAAACCTTGGGAAGGCAGTGGAAA	1803
Oy	600	AsnCysAlaArqLysLeuGlyPheThrGlnSerClnIleAspGluIleAspHisAspTyr	619
Db	1804	AACGTGGCCCAAGCTGGGCTTCACAGAGCTCAGATCGATGAATGACACATGACAT	1863
Oy	620	GluArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTyrValMetArgGlu	639
Db	1864	GAAGAGATGAGACGAAAGAGAAAGTTTACCAATGCTTCGAAAGTGGCTGATCGGGGAA	1923
Oy	640	GlyIleLysGlyAlaThrValGlyLysLeuAlaGlnIleAlaLeuHisGlnCysSerArgIle	659
Db	1924	GGCACCAAGGGGCGACAGTGGGAAAGTGGCCCAAGGACCTTCACCAATGTTGACAGATA	1983
Oy	660	AspLeuLeuSerSerLeuIleTyrValSerGlnAsn	671
Db	1984	GACCTGCTGACACCACTTGATTCGTGCGCACCGCCAGAC	2019
RESULT 7			
US-09-328-111-495			
Sequence 495, Application US/09328111			
Patent No. 6262333			
GENERAL INFORMATION:			
APPLICANT: Endege, Wilson O.			
APPLICANT: Steinmann, Kathleen E.			
APPLICANT: Astle, Jon H.			
APPLICANT: Burgess, Christopher C.			
APPLICANT: Bushnell, Steven E.			
APPLICANT: Carroll III, Eddie			
APPLICANT: Catino, Theodore J.			
APPLICANT: Derli, Adnan			
APPLICANT: Ford, Donna M.			
APPLICANT: Lewis, Marcia E.			
APPLICANT: Monahan, John E.			
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION			
FILE REFERENCE: CCD-257 (US)			
CURRENT APPLICATION NUMBER: US/09/328,111			
CURRENT FILING DATE: 1999-06-08			
EARLIER APPLICATION NUMBER: US 60/088,801			
EARLIER FILING DATE: 1998-06-10			
NUMBER OF SEQ ID NOS: 850			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 495			
LENGTH: 606			
TYPE: DNA			
ORGANISM: Homo sapiens			

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; FEATURE: misc_feature
; NAME/KEY: (1)...(606)
; LOCATION: (1)...(606)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-495

Alignment Scores:
Pred. No.: 5.89e-46 Length: 606
Score: 521.00 Matches: 99
Percent Similarity: 99.00% Conservative: 0
Best Local Similarity: 99.00% Mismatches: 1
Query Match: 14.70% Indels: 0
DB: 4 Gaps: 0

US-09-981-397A-16 (1-671) x US-09-328-111-495 (1-606)
OY 572 TyGlnAlaIlePheAspThrTrpSerLeuThrAspGlyHisLeuAspProIleArg 59
Db 3 TACCACACTCTCTTGATATACCACTAGCTGACGATAAACACCTGGACCCATCAGG 62
OY 592 GlnAsnLeuGlyHisTrpLysAsnCysAlaArgLysLeuGlyPheThrGlnSerGln 61
Db 63 GAAATCTGGGAAAGCAGCTGGAAGAACTGCGCCGTAACCTGGGCTTACACAGCTCAG 122
OY 612 IleAspGluIleAspHisAspTrpGluArgAspGlyLeuLysGluLysValTrpGlnMet 63
Db 123 ATTGATCAAAATTCGACCTGACTATGAGCGAGATGACATGAAAGAAAGCTTTACCGATG 18
OY 632 LeuGlnIleTrpValMetArgGluGlyIleLysGlyValAlaThrValGlyLysLeuAlaGln 65
Db 183 CTCGAAAGAGGGGAGTGAAGGAGGATTAAGGAGCAGCGTGGGAGAGCTGGCCAG 24
OY 652 AlaLeuHisGlnCysSerArgIleAspLeuLeuSerSerLeuIleTrpValSerGlnAsn 67
Db 243 GCGCTCCACAGAGTTCCTCGATGACGACCTTGAGAGAGCTTATTAGGTACGACGAGAAC 30

RESULT 8
US-09-329-418-1
; Sequence 1, Application US/09329418
; Patent No. 6096539
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; FILE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM-70536
; CURRENT APPLICATION NUMBER: US/09/329,418
; CURRENT FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-329-418-1

Alignment Scores:
Pred. No.: 2.37e-37 Length: 1873
Score: 448.00 Matches: 153
Percent Similarity: 42.52% Conservative: 100
Best Local Similarity: 25.71% Mismatches: 187
Query Match: 12.64% Indels: 156
DB: 3 Gaps: 22

US-09-981-397A-16 (1-671) x US-09-329-418-1 (1-1873)
OY 1 MetGlnProAspMetSerLeuAsnValIleLys----- 11
Db 147 CTGGCACCCTTCGACCGCTGATGTGCTCGTCAAGTTATGGCCAGCGAGTCCGCCGCC 20
OY 12 MetLysSerIleAspPheLeuGlnIleSerAlaGluLeu---AspSerGlyGlyPheGlyLys 30
Db 207 TTGGTGTTCATCGAGGAACTGGGAGAACCGAGAGCTGTGCGCAAGAGCGGGTGGGACA 26
OY 31 ValSerLeuGlyPheHisArgThrGlnGlyLeuMetIleMetLysTrpValTrpLysGly 50

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Db      267  GTGTTCCGGGCAACATGAGAGTGGGC-----TACGATGTG 305
QY      51  ProAsnGlyIleGluHisAsnGluAlaLeuGluGluAlaLeuMetMetAsnArgLeu 70
Db      306  GCGGTCAAGATGCTGAATCTGAGAGGCGATATCCAGCGAGTCACAGCCATGGCAAGTGTG 365
QY      71  ArgHisSerArgValValLysLeuLeuGlyValIleIleGluGluGly-----86
Db      366  GATACGAATTCGTCTCGCTAGAGGGGTTATCGAGAGTGGCGGCGCTCCAGCCAA 425
QY      87  -----LysTyrSerLeuValMetLeuTyrMetGluLysGlyAsnLeuMetHisValLeu 104
Db      426  GATCCCAAGCCGGCTGTGTGATTAATTCATGAGGAACGGCTCTCTGCGGGGCTGTG 485
QY      105  LysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeuGluIleLeu 124
Db      486  CAGTCCCAAGTCCCTCGGCGCTGGCCGCTCTTTCGCGCTGTGAAGAAGTGGTGT 545
QY      125  GlyMetCysTyrLeuHisGlyLysGly-----ValIleHisLysAspLeuLysProGlu 142
Db      546  GGGATGTTTACCTGACACCGACCAACCGGTCCTGCAACCGGAGCTCAAGCCATCC 605
QY      143  AsnIleLeuValAspAsnAspPheHisIleLeuIleAlaAspLeuGlyLeuAlaSerPhe 162
Db      606  AACGTCCTGTGGACCCAGACCTGCACGTCAAGCTGCAGATTTGGCGCTCCACATTT 665
QY      163  LysMetTrpSerLysLeuAsnAsnGluHisAsnGluValArgGluValAlaAspLys 182
Db      666  CAGGAGGCTCACAG-----TCAGGACA 689
QY      183  AlaLys---LysAsnGlyLysThrLeuTyrTyrMetAlaProGluHisLeuAsnAspVal 201
Db      690  GGGTCGGGGGCGGCGGCGACCTCGGCTACTGTCGCACTTTGTTGTTAACTGA 749
QY      202  AsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValAlaLeuTrpAlaLe 221
Db      750  AACCGGAAGGCTCTCCACAGCAGGTACGTACACTTGGAGTTCATGTGGGCACTG 809
QY      222  PheAlaAsnLysGlu-----ProTyrGlu-----AsnAlaIleCys 233
Db      810  CTTCGTGAGAGAGAAGTGTGAGTTCGCAACCGACCATCTGCTGTACGAGCACTGTCC 869
QY      234  GluGluGluLeuIleMetCysLysLysSerGlyAsnArgProAspValAspAspIleThr 253
Db      870  AACAGGCGAG-----AACCGGCTTTCATGGCTGAGACTGCC 905
QY      254  GluTyrCysProArgGlu-----IleIleSerLeuMetLysLeuCysTrp 268
Db      906  CAAAGCGGGGCTGTAGACTCCCGGCTTGTAGAGACTGAAGAGACTATGCTGCTGG 965
QY      269  GluAlaAsnProGluAlaArgProThrPhe-----ProGlyIleGluLys 284
Db      966  AGCAGTAGAGCCCAAGAGACACCTCTCCAGAGATCCCTACCAAAACATGATCAATC 1025
QY      285  PheArgProPheTyrLeuSerGluLeuGluLysSerValGluGluAspValLysSerLeu 304
Db      1026  TTCCAG-----ATGCTGAGCAACAATATGATGCTGCTCCACGGSTA 1070
QY      305  LysLysGluTyrSerAsnGluAsnAlaValAlaValLysArgMetGlnSerLeuGlnLeuAsp 324
Db      1071  AAGGATTTCCCTGTCTGCTACGCTAGAGACGACATATGAGCATTT-----1112
QY      325  CysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnProGlySerLeuHis 344
Db      1113  -----TCTATCCAGAGTCA-----1127
QY      345  SerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaProSerLeuGlu 364
Db      1128  -----GGCCAAGAGGAGGAGCAAAATGATGCTTTAGAGAACCATAGAA 1172
QY      365  HisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyr 384

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Db      1173  AACCAAGACACTGCTGTAATGATGATGCTGTTCTGAGTGTCTA-----1214
QY      385  HisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAla 404
Db      1215  -----AACAACTGATCTAGAGAGGACCTCCAGCTGTGT-----1250
QY      405  TyrAsnArgGluGluGluArgArgArgValSerHisAspProPheAlaGlnArg 424
Db      1251  -----CCTAA-AAATCCCCAG 1267
QY      425  ProTyrGluAsnPheGlnAsnThrGluLysGlyThrValTyrSer-SerAlaAlaSer 444
Db      1268  CCTTACCAAGAGGAGACAGGAGCAAGAGACAGAGCTTCCACAGCTTGACAGGAGCAC 1327
QY      444  HisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlu 464
Db      1328  ATCTTCAGATTCGATGGCCCAACT-----CCCCAGACTCCAGAGACTCAACTTT 1378
QY      464  AsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAl 484
Db      1379  CAGAAACCAAGATGCCAC-----CCTACCTCACTGGAGACA--1415
QY      484  ArgProArgValTrpTyrArgProIleProSerHisMetProSerLeuHisAsnIlePr 504
Db      1416  -----CCAAGT-----CC 1423
QY      504  GValProGlnThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuProPr 524
Db      1424  TGGACCCCGAGGAGTACAGGGGGCTGAGAGACAAAGCATGACTGTGCTCCAGAGCCCC 1483
QY      524  OThrAspGluSerIleLys-----TyrThrIleTyrAsnSerThrGlyIleGlu 540
Db      1484  GGAGCCAATCTCAGTAACAGGAGCGACCGCTCGTTAACATATATCAACTGCTCGGGGTCA 1543
QY      540  nIleGlyAlaTyrAsnTyrMetGluIleGlyLysSerSer 554
Db      1544  AGTTGGAGACAACAACACTTGTGACTATGCAACAGACAACTGCC 1586

RESULT 9
US-09-531-914-1
; Sequence 1, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531,914
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-531-914-1

Alignment Scores:
Pred. No.: 2.37e-37 Length: 1873
Score: 448.00 Matches: 153
Percent Similarity: 42.52% Conservative: 100
Best Local Similarity: 25.71% Mismatches: 187
Query Match: 12.64% Indels: 156
DB: 4 Gaps: 22

US-09-981-397A-16 (1-671) x US-09-531-914-1 (1-1873)
QY      1  MetGlnProAspMetSerLeuAsnValIleLys-----11
Db      147  CTGGCACCCTTCCAGCCTGATGTCTGCGCTCAAGTTATAGCCCGACGGGTGCCCCCCCC 206
QY      12  MetLysSerSerAspPheLeuGluSerAlaGluLeu---AspSerGlyGlyPheGlyLys 30

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Db      207 TTGGTGTCCATCGAGAGACTGGAGAACAGAGCTCTCGGCAAGCGCGGTTGGGACA 266
      31 ValSerLeuGlyPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGly 50
      267 GTGTTCGGGGCGGCAACATAGGAAGTGGGGC-----TAGCATGTG 305
      51 ProAsnGlyIleGlnHisAsnGlnAlaLeuLeuGlnGlnAlaLysMetMetAsnArgLeu 70
      306 GCGGTCAAGATCGTAACGTCAAGCGATATCCAGGAGGTCAGAGGCGCATCGCAAGTGTG 365
      71 ArgHisSerArgValValLysLeuLeuGlyValIleIleGlnGlyGly----- 86
      366 GATACCAATTCGTGCGCGCTTAGAAGGGTATTCAGAAAGTCGCGGGCTCGAGCCAA 425
      87 -----LysTyrSerLeuValMetGlnTyrMetGlnLysGlnAsnLeuMetHisValLeu 104
      426 GATCCCAAGCGCGGTCTGTGACTAAATTCATGGAGAACGGCTCTGTGTGCGGGCTGTG 485
      105 LysAlaGlnMetSerThrProLeuSerValLysGlyArgIleIleLeuGlnIleGln 124
      486 CAGTCCCAAGTCCCTGGCCCTGGCGCTCTCTGGCGGCTCGAAGAAGTGTGTG 545
      125 GlnMetCysTyrIleuHisGlyLysGly-----ValIleHisLysAspLeuLysProGln 142
      546 GGGATGTTTACCTACCGACAGAACACCGGCTGCTCTCGACCGGAGCATCAACCATCC 605
      143 AsnIleuValAspAsnAspPheHisIleLysIleLeuAspLeuGlnLysLeuAlaSerPhe 162
      606 AACCTCTGCTGGAGCCAGAGCTGCACGTCAAGCTGAGATTTGGCTCTCCACATTT 665
      163 LysMetThrSerLysLeuAsnAsnGlnGlnHisAsnGlnLeuArgGlnValAspGlyThr 182
      666 CAGGAGGCTCACAG-----TCAGGAGCA 689
      183 AlaLys---LysAsnGlyGlyThrLeuTyrTyrMetAlaProGlnHisLysAsnAspVal 201
      690 GGGTCCGGGAGGAGGCGGAGCCCTGGCTACTTGGCCAGAACGTTTGTTAACGTA 749
      202 AsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValAlaLeuThrAlaIle 221
      750 AACCGGAAGGCTCTCACAGCCAGTACGCTTACAGCTTCCGGATCTTAATGTGGGACGTG 809
      222 PheAlaAsnLysGln-----ProTyrGln-----AsnAlaIleCys 233
      810 CTTCCTGGAGAGAGAGTGAAGTTCACACGAAACCATCATCTGCTACAGAGAGCTGTCC 869
      234 GlnGlnGlnLeuIleMetCysIleLysSerLysAsnArgProAspValAspAspIleThr 253
      870 AACAGGCGAG-----AACCGGCTTCAATTGGCTGAGACTGCC 905
      254 GlnTyrTyrProArgGln-----IleIleSerLeuMetLysLeuCysTrp 268
      906 CAACCCGGGCTCGAGACTCCCGGCTTAGAAGAGCTGAAGAGCAATATGCTGCTCCACGTA 965
      269 GlnAlaAsnProGlnAlaArgProThrPhe-----ProGlnIleGlnGlnLys 284
      966 AGCAGTGAAGCCCAAGACAGACCCCTCTCCAGCAATGCCCTACCAAAAACATGATGAAGTC 1025
      285 PheArgProPheTyrLeuSerGlnLeuGlnGlnSerValGlnGlnAspValLysSerLeu 304
      1026 TTCAG-----ATGCTGAGAGAACATATGATGCTGCTGCTCCACGTA 1070
      305 LysLysGlnTyrSerAsnGlnAsnAlaValValLysLysMetGlnSerLeuGlnLeuAsp 324
      1071 AAGGATTTCTCTGCTCAGCTCAGAGCAAGCAATATGGAGATTT----- 1112
      325 CysValAlaValProSerSerArgSerAsnSerAlaThrGlnGlnProGlySerLeuHis 344
      1113 -----TCATACCCAGAGTCA----- 1127
      345 SerSerGlnGlyLeuGlyMetGlyProValGlnGlnSerTrpPheAlaProSerLeuGln 364

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Db      1128 -----GCCCAAGAGGAGACAGAAATGATGGCTTTAGAGAACCATAGAA 1172
      365 HisProGlnGlnGlnAsnGlnProSerLeuGlnSerLysLeuGlnAsnGlnAlaAsnTyr 384
      1173 AACGAGACACTCTGTAATGATGATGATGTTTCTAGTGGCTA----- 1214
      385 HisLeuTyrGlySerArgMetLysAspArgGlnThrLysGlnGlnProArgGlnAsnValAla 404
      1215 -----AACAACTGATCTAGAGAGGAGGCTCCACAGTCTGTT--- 1250
      405 TyrAsnArgGlnGlnGlnArgArgArgValSerHisAspProPheAlaGlnGlnArg 424
      1251 -----CCTAA-AAATGCCGAG 1267
      425 ProTyrGlnAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSer-SerAlaIle 444
      1268 CTTTACCAAGAGGAGGAGGACAGAGAGAGAGAGAGTTCACAAACCTGGAGAGGAGCAC 1327
      444 HisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGln 464
      1328 ATCTTCAGATTCGATGGCCCAACT-----CCCAAGACCTCCAGAGACTCAACTTT 1378
      464 AsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAla 484
      1379 CAGAAACAGATGCGCCAGC-----CCTACCTCAACTGGAGACA-- 1415
      484 aglyProArgValTrpTyrArgProIleProSerHisMetProSerLeuHisAsnIlePr 504
      1416 -----CCAAGT-----CC 1423
      504 ovalProGlnThrAsnTyrLeuGlnLysAsnThrProThrMetProPheSerSerLeuProPr 524
      1424 TGGACCCCGAGGAGATCAGGGGCGCTGAGAGACAGAGCATGACGTCTCCAGAGACC 1483
      524 cThrAspGlnSerLys-----TyrThrIleTyrAsnSerThrGlyIleGln 540
      1484 GGAGCCAAATCCAGTATACAGAGGCGAGCCGCTGTTAAATACATGACATGCTCTGGGTGCA 1543
      540 nileGlyAlaTyrAsnTyrMetGlnIleGlyGlyThrSerSer 554
      1544 AGTTGAGACACAACTACTTGTACTATGCAACAGACAACTGCC 1586

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RESULT 10
 US-09-329-418-2
 : Sequence 2, Application US/09329418
 : Patent No. 6096539
 : GENERAL INFORMATION:
 : APPLICANT: ZENECA Limited
 : TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
 : FILE REFERENCE: PHM.70536
 : CURRENT APPLICATION NUMBER: US/09/329,418
 : CURRENT FILING DATE: 1999-06-11
 : NUMBER OF SEQ ID NOS: 39
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 2
 : LENGTH: 1557
 : TYPE: DNA
 : ORGANISM: Homo Sapiens
 US-09-329-418-2

Alignment Scores:
 Pred. No.: 2,79e-37 Length: 1557
 Score: 446.00 Matches: 150
 Percent Similarity: 43.01% Conservative: 96
 Best Local Similarity: 26.22% Mismatches: 181
 Query Match: 12.58% Indels: 146
 DB: 3 Gaps: 21

US-09-981-397a-16 (1-671) x US-09-329-418-2 (1-1557)

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      14 SerSerAspPheLeuGlnSerAlaGlnLeu---AspSerGlyGlyPheGlyLysValSer 32
      49 TCATCGAGAGAACTGGAGAACAGAGAGCTGCTGGCAAGGCGGCTTCGCGACAGTGTTC 108

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OY 33 LeucySpheHsArgThrGlnGlyLeuMetIleMetLysThrValTyrIleLysGlyProAsn 52
Db 109 CGGCGCAACATAGAGAGTGGGC-----TACATGTGGCGGTC 147
OY 53 CysIleGlnHisAsnGlnAlaLeuLeuGlnGlnAlaLysMetMetAsnArgLeuArgHis 72
Db 148 AAGATCGTAAACTCCAGGCGCATATCCAGGAGGTTCAGGCGCATAGGCGCAAGTGTGATTAAC 207
OY 73 SerArgValAlaValLeuLeuGlnValIle-----IleGlnGlnLys 87
Db 208 GAATTCGTGCTGCGCTAGAGAGGTTATCGAAGGTAAGTACGTGGACCAATCCACAG 267
OY 88 TyrSerLeuValMetGlnTyrMetGlnLysGlnAsnLeuMetHisValLeuLysAlaGln 107
Db 268 CCGGCTGTGTCGACTAAATTTCATGGAGAAGCGCTCTGTGCGGGCTGCTGACAGTCCAG 327
OY 108 MetSerThrProLeuSerValLysGlyArgIleIleLeuGlnIleIleGlnLysMetCys 127
Db 328 TGCCCTGAGCCCTGGCCGCTCTTTCGCGCTGTGAAGAGTGTGCTTGGATGTTT 387
OY 128 TyrLeuHisGlyLysGly-----ValIleHisAspLeuLysProGlnAsnIleLeu 145
Db 388 TACCTGCAGACACCAACCGGCTGCTGCGACCGGAGCTTAACCATCCACATCTCTG 447
OY 146 ValAspAsnAspPheHisIleLysIleAlaAspLeuGlnLysLeuAlaSerPheLysMetTrp 165
Db 448 CTGGACCCAGAGCTCAGCTCAAGCTGCGCATTTGGCTGTCCACATTCAGGAGAGC 507
OY 166 SerLysLeuAsnAsnGlnGlnHisAsnGlnLeuArgGlnValAspGlyThrAlaLys--- 184
Db 508 TCACAG-----TCAGGACAGGCGTCCGG 531
OY 185 LysAsnGlnGlyThrLeuTyrTyrMetAlaProGlnHisLeuAsnAspValAsnAlaLys 204
Db 532 GAGCAGAGGGGAGCGCTGGCTACTGGCCCGACAGACTGTTGTTAAGCTAAACCGGAG 591
OY 205 ProThrGlnLysSerAspValTyrSerPheAlaValValLeuTrpAlaIlePheAlaAsn 224
Db 592 GCCTTCACAGCAGTACGCTACAGCTCGGATCTAATGTGGGAGTCTGCTCGA 651
OY 225 LysGln-----ProTyrGln-----AsnAlaIleCysGlnGln 236
Db 652 AGAGAGTGTGAGTGTCCACACCAACCACTGCTGACGAGAGTGTGCAACCGAG 711
OY 237 LeuIleMetCysIleLysSerGlnAsnArgProAspValAspAspIleThrGlnLysCys 256
Db 712 -----AACGGCTTATTTGGCTGAGACTGCCCAACCGGG 747
OY 257 ProArgGln-----IleIleSerLeuMetLysLysCysTrpGlnAlaAsn 271
Db 748 CCTGAGACTCCCGGCTTAGAAGAGTGAAGAGCTAATGACAGCTGCTGAGAGCTGAG 807
OY 272 ProGlnAlaArgProThrPhe-----ProGlnIleGlnGlnLysPheArgPro 287
Db 808 CCCAAGGACAGACCTCTCTCAGAGATGCTTACCCAAAACATGATGATGATGCTCAG--- 864
OY 288 PheTyrLeuSerGlnLeuGlnLysSerValGlnGlnAspValLysSerLeuLysGln 307
Db 865 -----ATGCTGAGAGACATATGATGCTGCTGCTCCACGTTAAGATTTTC 912
OY 308 TyrSerAsnGlnAsnAlaValAlaValLysArgMetGlnSerLeuGlnLeuAspCysValAla 327
Db 913 CTGCTCAGCTCAGAGCAGACGATAGAGATTT-----TCT 948
OY 328 ValProSerSerArgSerAsnSerAlaThrGlnGlnProGlnSerLeuHisSerSerGln 347
Db 949 ATCCAGAGTCA----- 960
OY 348 GlnLeuGlnMetGlyProValGlnGlnLysSerThrPheAlaProSerLeuGlnHisProGln 367
Db 961 -----GGCCAAAGAGGAGCAGAAATGATGATGCTTTAGACAGAACCATGAAAAACAGCAC 1014

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OY 368 GlnGlnAsnGlnProSerLeuGlnSerLysLeuGlnAspGlnAlaAsnTyrHisLeuTyr 387
Db 1015 TCTCGTAATGATGTCATGTTCTGTAGTGGCTA----- 1047
OY 388 GlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArg 407
Db 1048 -----AACAACTGAATCTAGAGGAGCCTCCAGCTGTT----- 1083
OY 408 GlnGlnGlnArgArgArgValSerHisAspProPheAlaGlnGlnArgProTyrGln 427
Db 1084 -----CTTA-AAAATGCCGAGGCTTATCCAA 1109
OY 428 AsnPheGlnAsnThrGlnGlnLysGlyThrValTyrSer-SerAlaAlaSerHisGlyAs 447
Db 1110 GAGGAGCAGGCGCACAAGAGACGAGTTCACAGCTGAGACAGCAGCAGCATTTCCAGA 1169
OY 447 nAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAsnArg 467
Db 1170 TTGCAATGGCCCAACT-----CCCGAGACTCAGAGACCTCACTTCAGAAACCA 1220
OY 467 yLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlnThrAlaGlyProArg 487
Db 1221 GATGCCAGC-----CTTACTCACTGAGACA----- 1248
OY 487 gValTrpTyrArgProIleProSerHisMetProSerLeuHisAsnIleProValProGln 507
Db 1249 -----CCAGT-----CTGGACCCCG 1265
OY 507 uThrAsnTyrLeuGlnLysAsnThrProThrMetProPheSerSerLeuProProThrAspGln 527
Db 1266 AGGGAATCAGGGGCTGAGACAGCAGCATGACAGTGTGTCGACAGACCCGAGCCCAA 1325
OY 527 uSerIleLys-----TyrThrIleTyrAsnSerThrGlyIleGlnIleGlyAl 543
Db 1326 TCACATACAGAGGCGCAGCGCTCGTTAATACATATACACTGCTGTGGGTGTCANATTGGAGA 1385
OY 543 aTyrAsnTyrMetGlnIleGlyGlyThrSerSer 554
Db 1386 CAACAACACTTACTGACTATGCAACAGACAACTGCC 1419

RESULT 11
US-09-531-914-2
; Sequence 2, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531.914
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1557
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-531-914-2

Alignment Scores:
Pred. No.: 2,796-37 Length: 1557
Score: 446.00 Matches: 150
Percent Similarity: 43.01% Conservative: 96
Best Local Similarity: 26.22% Mismatches: 181
Query Match: 12.36% Indels: 146
DB: 4 Gaps: 21

US-09-981-397a-16 (1-671) x US-09-531-914-2 (1-1557)
OY 14 SerSerAspPheLeuGlnSerAlaGlnLeu-----AspSerGlyGlyPheGlyLysValSer 32
Db 49 TCCATCGAGGAACCTGAGACACCGAGCTCTCGCAAAAGCGGGTTTCGACAGCTTTC 108

```



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OY 33 LeucSpheHsArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGlyProAsn 52
    |||||
Db 109 CGGGCGCAACATAGAGAGTGGGC-----TTCGATGTGGCGCTC 147
OY 53 CysIleGluHisnGlnAlaLeuLeuGlnAlaLysMetMetAsnArgLeuArgHis 72
    ||| : : : : : ||| : : : : : ||| : : : : :
Db 148 AAGATCGTAACCTGAGAGCGGATATCCAGGAGAGTCAAGGCATGGCAAGCTCGATAC 207
OY 73 SerArgValValLysLeuLeuGlyValIle-----IleGluGluGlyLys 87
    ||| : : : : : ||| : : : : : ||| : : : : :
Db 208 GAATTCCTGCTGCGCTGAGAGAGGGGTATCGAGAGGTGAACCTGGACCAAGATCCCAAG 267
OY 88 TyrSerLeuValMetGluTyrMetLysGlyLysnLeuMetHisValLeuLysAlaGlu 107
    : : : : : ||| : : : : : ||| : : : : :
Db 268 CCGGCTGTGGTACATATTCATATGAGACAGCGCTCTGGCGGCTGCTGCATCCAG 327
OY 108 MetSerThrProLeuSerValLysGlyArgIleIleLeuGluIleIleGluGlyMetCys 127
    ||| : : : : : ||| : : : : : ||| : : : : :
Db 328 TGGCCCTGGCCCTGGCGCTCCCTTGGCTGTAAGAAGTGGTGGATGCTTT 387
OY 128 TyrLeuHisGlyGly-----ValIleHisLysAspLeuLysProGluAsnIleLeu 145
    ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db 388 TACCTGCACGACAGAACCCGCGTCTCTCCACCGGACCTCAAGCCATCCACGTCCTG 447
OY 146 ValAspAsnAspPheHisLysIleAlaAspLeuLysLeuAlaSerPheLysMetTrp 165
    : : : : : ||| : : : : : ||| : : : : :
Db 448 CTGACACCCAGAGCTGCACGCTCAGAGCTTGGCTGCTCCACATTTCCAGGAGGC 507
OY 166 SerLysLeuAsnAsnGlnGluHisnGluLeuArgLysValAspGlyThrAlaLys--- 184
    ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db 508 TCACAG-----TCAGGACAGAGGTCGGCG 531
OY 185 LysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspValAsnAlaLys 204
    : : : : : ||||| : : : : : ||||| : : : : :
Db 532 GAGCCAGGCGGACCCCTGGGCTACTTGGCCCCAGAACCTGTTTAACTGAACCGGAG 591
OY 205 ProThrGluLysSerAspValTyrSerPheAlaValLeuValIlePheAlaAsn 224
    : : : : : ||||| : : : : : ||||| : : : : :
Db 592 GCTCCACAGCCAGTACGCTACAGCTTGGGATCTTAATGTGGGAGTGGCTTGTGGA 651
OY 225 LysGlu-----ProTyrGlu-----AsnAlaLysGlyGluGln 236
    : : : : : ||| : : : : : ||| : : : : :
Db 652 AGAGAATGTAGTTCACCAACGCAACATCATCTGTACAGAGAGTGTGCACAGGCGAG 711
OY 237 LeuIleMetCysIleLysSerGlyAsnArgProAspValAspIleThrGlyCys 256
    ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db 712 -----AACCGGCTTCATTGGCTGAGCTGCCCAAGCCGG 747
OY 257 ProArgGlu-----IleIleSerLeuMetLysLysCysTrpGluAlaAsn 271
    ||| : : : : : ||||| : : : : : ||||| : : : : :
Db 748 CTGAGAGCTCCCGGCTTAGAAGACGTGAGAGCTTAATGAGCTCTCTCAGAGCAGTGA 807
OY 272 ProGluAlaArgProThrPhe-----ProGlyIleGlnGluLysPheArgPro 287
    ||| : : : : : ||||| : : : : : ||||| : : : : :
Db 808 CCCAAGACAGACCTCTCTCCAGAGATGCCCTACCAAACTGATGAAGTCTTCAG--- 864
OY 288 PheTyrLeuSerGlnLeuGlnSerValGlnLysPvalLysSerLeuLysGlu 307
    : : : : : ||| : : : : : ||| : : : : :
Db 865 -----ATGCTGAGAGAACATATGATATGCTCTCTCCAGGTAAGAGATTTC 912
OY 308 TyrSerAsnGlnLysnAlaValValLysArgMetGlnSerLeuGlnLeuAspCysValAla 327
    ||| : : : : : ||||| : : : : : ||||| : : : : :
Db 913 CTGCTCTAGCTCAGAGACCAATAGAGATT---TCT 948
OY 328 ValProSerSerArgSerAsnSerAlaThrGluGlnProGlySerLeuHisSerSerGln 347
    : : : : : ||| : : : : : ||| : : : : :
Db 949 ATCCCAAGTCA----- 960
OY 348 GlyLeuGlyMetGlyProValGluGluSerTrpPheAlaProSerLeuGlnHisProGln 367
    ||| : : : : : ||||| : : : : : ||||| : : : : :
Db 961 -----GGCCAAGAGGAGGAGAAATGATGAGCTTTAGAGAACCATAGAAACCAACAGC 1014

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OY 368 GluGluAsnGluProSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHisLeuTyr 387
    ||||| : : : : : ||| : : : : :
Db 1015 TCTCGTATATGATGATCATGCTTTCTGACTGGCTA----- 1047
OY 388 GlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArg 407
    : : : : : ||||| : : : : : ||||| : : : : :
Db 1048 -----AACCAACTGAACTAGAGGAGGCTCCAGCTCTGTT----- 1083
OY 408 GluGluGluArgGluArgValSerHisAspProPheAlaGlnAlaGlyProTyrGlu 427
    ||| : : : : : ||| : : : : :
Db 1084 -----CCTAA-AAAATGCCGAGCCTTACCAG 1109
OY 428 AsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSer-SerAlaLysSerHisGlyAs 447
    ||| : : : : : ||| : : : : :
Db 1110 GAGAGCAGCAGGACCAAGAGAGGAGGTTCCAAAGCTGGACAGACGACATCTTCAGA 1169
OY 447 nAlaValHisGlnProSerGlyLeuThrSerGlnProGluValLeuTyrLysHisnAsnG 1467
    : : : : : ||||| : : : : : ||||| : : : : :
Db 1170 TTGCGATGGCCCAACT-----CCCAAGACTCCAGAGACCTCAACTTTCCAGAAACA 1220
OY 467 YLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAlaGlyProAr 487
    : : : : : ||| : : : : : ||||| : : : : :
Db 1221 GATGCCCGAGC-----CCTACCTCAACTGGAGACA----- 1248
OY 487 gValTrpTyrArgProIleProSerHisMetProSerLeuHisnIleProValProG 507
    ||||| : : : : : ||||| : : : : :
Db 1249 -----CCAGT-----CCTGAGACCCG 1265
OY 507 uThrAsnTyrLeuGlyLysnThrProThrMetProPheSerSerLeuProThrAspG 527
    ||| : : : : : ||| : : : : :
Db 1266 AGGGAATCAGAGGGGCTAGAGACAGACGATGACTGCTCCAGAGACCCCGAGCCAA 1325
OY 527 uSerIleLys-----TyrThrIleTyrAsnSerThrGlyIleGlnIleGlyAl 543
    : : : : : ||||| : : : : : ||||| : : : : :
Db 1326 TCCAGTACAGAGGCGGACCGCTCGTTAACAATATACAGCTGCTGGGCTGCAAGTTGGAGA 1385
OY 543 aTyrAsnTyrMetGluIleGlyLysThrSerSer 554
    ||||| : : : : : ||||| : : : : :
Db 1386 CAACACTACTGACTATGACACAGACACTGGC 1419

RESULT 12
US-09-188-930-257
: Sequence 257, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Ornust, Rene
: APPLICANT: Mutison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188,930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 257
: LENGTH: 3516
: TYPE: DNA
: ORGANISM: Mouse
US-09-188-930-257

Alignment Scores:
Pred. No.: 6,82e-33 Length: 3516
Score: 410.50 Matches: 164
Percent Similarity: 43.43% Conservative: 84
Best Local Similarity: 28.72% Mismatches: 209
Query Match: 11.58% Indels: 116
DB: 3 Gaps: 25

US-09-981-397a-16 (1-671) x US-09-188-930-257 (1-3516)

```

QY	14	SerSerAspPheLeuGlnUbeLserIaGlnUleuAspSerGlyGlyPheGlyIysValSerLeu	33
Db	58	GGCGGGAAATTCGACAGCCTGGAGAAAGGCGGCTTCGGCGAGGTGTAACAAG	117
QY	34	CysPheHisArgThrGlnGlyLeuMetIleMetLysThr	50
Db	118	GGCGGCAT-----GGCACTGGAAAGACTGGCGTCCGATCAAGTCTCG	162
QY	51	ProHisCys-----IleGlnHisAsnGlu-----AlaLeuGlnGluValIleLysMetMet	67
Db	163	CCCAAGCTTCGACGTGCACACAGGAGAACCAATGCAGCTCTCGAGCAACCTAAGAAGATG	222
QY	68	AsnArgLeuArgHisSerArgValIleLysLeuLeuGlyValIleIleLeuGlnGlyLys	87
Db	223	GAGATGGCCCAAGTCCGATACATTCCTGCTGTGACAGCATTCGCCAGAA-----CCT	276
QY	88	TyrSerLeuValMetGlnUtyrMetGlnGlyGlyAsnLeuMetHisValLeuLysAlaGln	107
Db	277	GTGCGGTGTGTCATGGATACATGAGACAGAGCTCCCTGGAAGAAGTGTGGCTGCAGAG	336
QY	108	MetSerThrProLeuSerValLysGlyArgIleIleLeuGlnUleIleGlnGlyMetCys	127
Db	337	---CCATTCCTCTGGGACCTCGCGCTTCCTGCATCTGTGACAGACACACCGTGGCATGAAC	393
QY	128	TyrLeuHis-----GlyLysGlyValIleHisLysAspLeuLysProGlnAsnIleLeu	145
Db	394	TTCTCTGCATTCGATGTCTCCGCCACTGCGACCTAGACCTAGACCTAAGGCCAGCAACCTCTG	453
QY	146	ValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPheLysMetTyr	165
Db	454	CTGAGTCCCCACTTACCATCTCAAGATTTCTTGACTTTGGGCTGGCC-----	498
QY	166	SerLysLeuAsnAsnGlnGlnHisAsnGlnLeuArgGluValAspGlyThrAlaLysLys	185
Db	499	---AAGTGCAAATGGCATGTCACACTCTCATGACCTCAGCATGATGAGGCGCTGTT	549
QY	186	AsnGlyGlyThrLeuTyrTyrMetAlaProGlnHisLeuAsnAspValAsnAlaLysPro	205
Db	550	-----GGTACATGAGCTTACTCTCCCTCCGAGAGCAATTCGTAGAAAGGCGCTGTTT	603
QY	206	ThrGlnLysSerAspValTyrSerPheAlaValIleLeuTyrAlaIlePheAlaAsnLys	225
Db	604	GACACCAAAACATGATGATACAGCTTCGCCATTTGATGTGGGCGTGTGCTTACACAGAG	663
QY	226	GluProTyrGlnAsnAlaIleCysGlnGlnGlnLeuMetCysIleLysSerGlyAsn	245
Db	664	AAGCATTTGGCAGATGAAGAAAGAAATCTCAACATCATGATGAAGTGTAAAGGGCCAC	723
QY	246	ArgProAspValAspAspIleThrGlnUtyrCysProArg-----GluIleIleSer	262
Db	724	GGCCCGAGAGCTGCCAACCCTATGCAAGACCCCGCGCGCTGTGCCAGCCTGTATAGG	783
QY	263	LeuMetLysLeuCysTyrPglValAsnProGlnUalArgProThrPheProGlyIleGln	282
Db	784	CTCATGGCAAGGTTGCTGGCATGCACACCCACAGGTCGGGCCACCTTCCAGAAATTTACC	843
QY	283	GlnUtyrPheArgProPheTyrLeuSerGlnGlnGlnUtyrSerValGlnGlnAspValLys	302
Db	844	TCTGAA-----ACAGAGACACCTTGTGAGAAACCGCATGACGAGAGGTAA	888
QY	303	SerLeuLysLysGlnUtyrSerAsnGlnAsnAlaValIleLysArgMetGlnSerLeuGln	322
Db	889	GACCTGGGCTCAGACCCAGCGCAGAAAGC-----TCTCTAGAG	927
QY	323	LeuAspCysValAlaValPro-----SerSerArgSerAsnSerAlaThrGlnGlnProGly	341
Db	928	TCCAAAGATGAGGCCAGGCCAGGCTCTACGCCCTCAAGCGCGCTGTCTCCGCCCTTC	987
QY	342	SerLeuHisSerSerGlnGlyLeuGlnUtyrGlyProValGlnGlnUtyrPheAlaPro	361
Db	988	GATACGCACTGCATCTCTCCGAGTGTGCGTACAGATTG---GACTCTGGAGTCTCCGAG	1044
QY	362	SerLeuGlnHisProGlnGlnGlnAsnGlnUProSerLeuGlnSerLysLeu---GlnAsp	380

[illegible]

Alignment Scores:

Pred. No.: 1,17e-29 Length: 1888
 Score: 375.50 Matches: 156
 Percent Similarity: 41.86% Conservative: 83
 Best Local Similarity: 27.32% Mismatches: 219
 Query Match: 10.59% Indels: 115
 DB: 3 Gaps: 26

US-09-981-397a-16 (1-671) x US-09-188-930-66 (1-1888)

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OY 14 SerSerAspHeuLeuGluSerAlaGluLeuAspSerGlyClyPheGlyLysValSerLeu 33
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
58 GCGCGCAATTCCTCCAGCTGGAGAAAGTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGACAG 117
OY 34 CysPheHisArgThrGlnGlyLeuMetLeuMetLysThr-----ValTyrLysGly 50
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
118 GTCCGCCAT-----GTGCACGTGAGACGTGGCTCCGCCGATCAAGTCTCG 162
OY 51 ProAsnGly-----IleGlnHisAsnGlu-----AlaLeuLeuGlnGlnAlaLysMetMet 67
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
163 CCCAGTCTGCACGTGCACGACGAGAAAGCAATGAGAGTCTCGGAGAGAGTAAAGATG 222
OY 68 AsnArgLeuArgHisSerArgValValLysLeuLeuGlyValIleIleGlnGlyLys 87
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
223 GAGATGGCCAGATTCGATCACTTACCTGTACGCGCATATGCCAGAA-----CCT 276
OY 88 TyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeuLysAlaGlu 107
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
277 GTCCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 336
OY 108 MetSerThrProLeuSerValLysGlyArgIleIleLeuGlnIleIleGlnGlyMetCys 127
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
337 ---CAATGGCTTGGGACCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 393
OY 128 TyrLeuHis-----GlyLysGlyValIleHisLysAspLeuLysProGlnAsnIleLeu 145
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
394 TTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 453
OY 146 ValAspAsnAspPheHisIle-----LysIleAlaAspLeuGlyLeuAlaSerPheLysMet 164
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
454 CTGGATGCCACACTACCAAAATGTCAGAGATTTCTTGACTTGGCTGGCTGGCTGGCTGGCTGGCT 501
OY 165 TrpSerLysLeuAsnAsnGlnGlnHisAsnGluLeuArgLysValAspGlyThrAlaLys 184
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
502 -----AAGTGCATATGCGATGCTCCACTGTACGATGACCTCAGCATGATGATGCTGCTT--- 552
OY 185 LysAsnGlyLysThrLeuTyrTyrMetAlaProGlnHisLeuAsnAspValAsnAlaLys 204
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
553 -----GGTCAATTCGGCTACCTCCCTCCCTCCAGAGCAATTCGTGAGAGAGCCGCTTG 603
OY 205 ProThrGluLysSerAspValTyrSerPheAlaValValLeuThrPheAlaIlePheAlaAsn 224
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
604 TTTCGACACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 663
OY 225 LysGluProTyrGlnAlaIleCysGlnGlnGlnLeuLeuMetCysIleLysSerGly 244
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
664 AATAATCCATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 723
OY 245 AsnArgProAspValAspAspIleThrGluTyrCysProArg-----GluIleIle 261
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
724 CACCGCCCAAGATGCTGCACGATCAGACCCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 783
OY 262 SerLeuMetLysLeuGlyTrpGlnAlaAsnProGlnAlaArgProThrPheProGlyIle 281
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
784 GGGCTATGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
OY 282 GlnGluLysPheArgProPheTyrLeuSerGlnLeuGlnGlnValGlnGlnVal 301
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
844 ACCTGTGA-----ACAGAAGACCTTTGTGAGAGAGCTGATGAGAGAGCTG 888
OY 302 LysSerLeuLysGlyTyrSerAsnGlnAsnAlaValValLysArgMetGlnSerLeu 321
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
889 AAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 927

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OY 322 GlnLeuAspCysValAlaValPro---SerSerArgSerAsnSerAlaThrGlnGlnPro 340
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
928 GAGTCCAGAGTGAAGGCGCCAGGCTCCATCCTCAGCGCTTCAAGCGCGCTGCTCCCGCC 987
OY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGlnGlnGlnSerThrPheAla 360
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
988 TTTCGATTAACGACCTCCTCTCTCCGACTTGTCTGATCAGATGTTGAGACTCTGGGATTTCCCA 1047
OY 361 ProSerLeuGlnHisProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 379
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1048 AGACTCTTGAAGGCGCCGAGAGAGCTCAGGAGTTCTCTGATATGATCAAGCTCCATCG 1107
OY 380 AspGlnAlaAsnTyrHisLeuTyrGly---SerArgMetAspArgGlnThrLysGlnGln 398
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1108 TCACGAGGAGCAAGAGCTCTCGGGGTCTGCTGATGATGATGATGATGATGATGATGATGATG 1167
OY 399 ProArgGlnAsnValAlaTyrAsnArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 418
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1168 GATCGCTGTGACATGCTCTTTGACGCGGAGGCTTC-AAACAGCGCA----- 1211
OY 419 ProPheAlaGlnGlnArgProTyrGlnAsnPheGlnAsnThrGlnGlyLysGlyThrVal 438
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1212 CCTGGGCCCCACAGACATCCAGAGAA-----GAAGCTAGCGATGCCAT 1256
OY 439 TyrSerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSer-----Gly 454
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1257 CAT-----ATCAGGAGACACACAGAGCTGATGATGATGATGATGATGATGATGATGATG 1310
OY 455 LeuThrSer----- 457
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1311 CTTCGTTCTAGACAGCAGTGCACAGCTGCTGACACTGCTGTGAGAGCCGAGACAGAGA 1370
OY 458 -----GlnProGlnValLeuTyrGlnAsnAsnGly 467
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1371 GTGTGTCAAGTGGCTGCTGCTTAAATGCCAACCCCAACT---GACCAACAGAGAGG 1427
OY 468 LeuTyr---SerSerHisGlyPheGlyThr----- 476
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1428 CTTCACACACTGCATATGCTGTGTGAGCGGAGAGGAGCTGGAATTTGGAGACTACTGCT 1487
OY 477 -----ArgProLeuAsp---ProGlyThrAla 484
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1488 AGCCCGGAGACAGCTGTCATGCGCAAGATGAAGACAGAGTGCCTGCTGCTGCTGCTGCTGCTG 1547
OY 485 GlyProArgValTyrTyrArgProIleProSerHisMetProSerLeuHisAsnIlePro 504
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1548 AGCCCAAAA---TGGGG-ATGAAGGCCAGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1603
OY 505 ValProGlnThrAsnTyrLeuGlyAsnThrPro 515
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1604 GTCAATGAGGTGAGCTTGAAGGCCGAACCC 1636

```

RESULT 14
 US-09-099-041A-3
 : Sequence 3. Application US/09099041A
 : Patent No. 6340576
 : GENERAL INFORMATION:
 : APPLICANT: Bertin, John
 : TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 : TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 : FILE REFERENCE: 07334-076001
 : CURRENT APPLICATION NUMBER: US/09/099, 041A
 : PRIOR FILING DATE: 1998-06-17
 : PRIOR APPLICATION NUMBER: 09/019, 942
 : NUMBER OF SEQ. ID NOS: 37
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 3
 : LENGTH: 1620
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-099-041A-3

Alignment Scores:

Pred. No.: 2,69e-29 Length: 1620
 Score: 371.00 Matches: 112
 Percent Similarity: 46.27% Conservative: 68
 Best Local Similarity: 28.79% Mismatches: 145
 Query Match: 10.47% Indels: 64
 Gaps: 12

US-09-981-397a-16 (1-671) x US-09-099-041a-3 (1-1620)

```

QY 23 Leuaspsergllygylphleglylvalserleucyspnehis-----ArgThrGln 39
Db 70 CTGAGCCGCGGCGCTGTGCGACTGTGTCGCCGCCGCCGACGAGACTGGCGCTCCAG 129
QY 40 Glyleumetilemetlythvaltyrlysglyproasnysileglnhisasnlguala 59
Db 130 ---GTGGCCGTGAAGACCTGCACATCCACACTCCGCTGCGACGACGAAAGAAAGCAT 186
QY 60 Leuleuglglualalysmetmetasnargleuarghisserargvalvalylsleu 79
Db 187 GTCTTAGAGAAAGCTGAATTTTACAAACCTAGATTGTTACATTCCTTCCAAATTTTG 246
QY 80 Glyvallelleleuglgluglyltyrserleuvalmetglutyrmetsglulysasn 99
Db 247 GGAATTTGCATGAGCCTGAAATTTTGGGAATGCTTACTGATACATGCCAAATGATCA 306
QY 100 Leumethisvalleuylsalaglumetserthrpro-----LeuserValylsgly 116
Db 307 TTAATGAACTCTCTACATAGAGAAACGAAATATCTTGATGTGCTGGCCCTTAGATTT 366
QY 117 Argillelleleuglglulleleuglymetcystyryleuhsigly----LysglyVal 134
Db 367 CGCATCTCTGCAATGAAATTTGCCCTGTGTAATTAATTCGCAATATGACTCTCTCTTA 426
QY 135 Ilehislyaspseuylsprogiluasnilleuvalaspaasnprnehisilelystle 154
Db 427 CTTCATCATGACTCTGAGACTCAGAAATATCTTATTGGCAATGAAATTTCAATGTTAA 486
QY 155 Alaaspseuylleuvalaserpseuylmetrserlyseuasnlglnhisasn 174
Db 487 GCAGATTTTGGTTATCAAGTGGCGCATGTGCTCCCTCAGACGTACAGAAAGTACAA 546
QY 175 GluleuarggluvalaspglythrAlalyslsasnlglythrleuTYTYrmetala 194
Db 547 TCTGCACACAGAA-----GGAGGCGCAATTAATCTATATGCCA 582
QY 195 Progluhsleuasnaspvalasnalalysprothrghluysser----- 209
Db 583 CCTGAA-----AACTATGAACCTGACAAATAATCAAGGCCAGTATGACG 627
QY 210 ---AspValtyrSerphealavalalleuThrAlallephealaaasnlgulprotyr 228
Db 628 CACGATATATATACCTATGACGTATGATCAATGGAGATGTTATCCAAAAAACACCTTT 687
QY 229 Gluasnalallecysgluglnleuileuilemetcystleuysserglyasnargproasp 248
Db 688 GAAGATGTCACCAATCTTGTGCATATATATAGTGTGTCCACAAAGACATCGACGTGT 747
QY 249 ValaspseuyllethrghluTYrCysProarglulile-----IleSer 262
Db 748 ATTAATGAA-----GAAGTTTGGCCATGATGATATACCTACCGACGACGATGATCT 801
QY 263 LeumetlyseuTYrTPglualalasnproglualaargprothrpherglylleglu 282
Db 802 CTATATAGAAAGTGATGGCAACAATTCAGATGAAGACCATCTTCTTAATAATGTTTA 861
QY 283 GlulysheargpropheryrleuSerleuGluegluluserValgluluaspyalys 302
Db 862 ATAGAACTTGACACCTTTTGAGAAACATTTGAGAGATTAATCTTTCTTGAAGCTGTAT 921
QY 303 Serleuylslysglutyryserasnlgualavalvalylsalargmetglnserleu 322
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Db 922 CAGCTAAGAA-----ACAAAGTTACAGATGTT--- 951
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QY 343 LeuhsisserglnglyleuglymetglprovalglugluserTYrThrphalaproser 362
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QY 363 Leucluhis-----Proglngluasnlglu 371
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QY 372 Proserleuglnserlyslsleuasp 380
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RESULT 15

US-09-245-281-3

Sequence 3, Application US/09245281

Patent No. 6369196

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

FILE REFERENCE: 0734/118001

CURRENT APPLICATION NUMBER: US/09/245,281

EARLIER FILING DATE: 1999-02-05

EARLIER FILING DATE: 1998-12-08

EARLIER APPLICATION NUMBER: US 09/099,041

EARLIER FILING DATE: 1998-06-17

EARLIER APPLICATION NUMBER: US 09/019,942

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FASTED for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1620

TYPE: DNA

ORGANISM: Homo sapiens

US-09-245-281-3

Alignment Scores:

Pred. No.: 2,69e-29 Length: 1620
 Score: 371.00 Matches: 112
 Percent Similarity: 46.27% Conservative: 68
 Best Local Similarity: 28.79% Mismatches: 145
 Query Match: 10.47% Indels: 64
 Gaps: 12

US-09-981-397a-16 (1-671) x US-09-245-281-3 (1-1620)

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Db 130 ---GTGGCCGTGAAGACCTGCACATCCACACTCCGCTGCGACGACGAAAGAAAGCAT 186
QY 60 Leuleuglglualalysmetmetasnargleuarghisserargvalvalylsleu 79
Db 187 GTCTTAGAGAGAGCTGAATTTTACAAACGTAAGATTGTTACATTCCTTCCAAATTTTG 246
QY 80 Glyvallelleleuglgluglyltyrserleuvalmetglutyrmetsglulysasn 99
Db 247 GGAATTTGCATGAGCCTGAAATTTTGGGAATGCTTACTGATACATGCCAAATGATCA 306
QY 100 Leumethisvalleuylsalaglumetserthrpro-----LeuserValylsgly 116
Db 307 TTAATGAACTCTCTACATAGAGAAACGAAATATCTGATGTGCTTGGCCATGAGATTT 366

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OY 117 ArgIleIleLeuGluIleIleGluIleMetCysTyrLeuHisGly-----LysGlyVal 134
DB 367 CGCATCTGCATGAATGTCCTTGTTGTAATTAACCTGCACATATGACTCTCCTTTA 426
OY 135 IleHisLysAspLeuLysProGluAsnIleLeuValAspAsnAspPheHisIleLysIle 154
DB 427 CTTTCATCATGACTGACAGACCTGAAATATCTTATGTGACAAATGAATTCATCTTAAGATT 486
OY 155 AlaAspLeuGlyLeuAlaSerPheLysMetTrpSerLysLeuAsnAsnGluGluHisAsn 174
DB 487 GCAGATTGTTGGTTTTCAAAGTGGCGCATGATGCCCTCTCACAGTCACGAAGTAGCANA 546
OY 175 GluLeuArgGluValAspGlyThrAlaLysLysAsnGlyGlyThrLeuTyrTrpMetAla 194
DB 547 TCTGCACCCAGAA-----GGAGGACAAATTATCTATATGCCA 582
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DB 688 GAAGATGTCACCAATCCTTGGCAGATATATGATAGTGTGCACAAAGACATGACCTGTT 747
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DB 748 ATTAATGAA-----GAAAGTTGGCATATGATATACCTCACCGAGCAGTATGATCTCT 801
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Search completed: June 25, 2003, 22:32:20
Job time : 154 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame-plus.p2n model

Run on: June 25, 2003, 21:59:04 ; Search time 239 Seconds
(without alignments)
4119.848 Million cell updates/sec

Title: US-09-981-397A-16
Perfect score: 3545
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Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1042519 segs, 733713590 residues
Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=Numa40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3545	100.0	2617	9	US-09-981-397A-15
3	772	21.8	529	9	US-09-854-133-676
4	641	18.1	392	9	US-09-918-995-17425

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7	521	14.7	606	10 <td>US-09-879-536-495</td> <td>Sequence 495, App</td>	US-09-879-536-495	Sequence 495, App	
8	463	13.1	430	10 <td>US-09-960-352-4340</td> <td>Sequence 4340, Ap</td>	US-09-960-352-4340	Sequence 4340, Ap	
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10	440	12.4	1697	10 <td>US-09-862-027-7</td> <td>Sequence 1, App11</td>	US-09-862-027-7	Sequence 1, App11	
11	410.5	11.6	2370	9 <td>US-10-164-080-1</td> <td>Sequence 1, App11</td>	US-10-164-080-1	Sequence 1, App11	
12	410.5	11.6	2370	9 <td>US-10-299-327-1</td> <td>Sequence 1, App11</td>	US-10-299-327-1	Sequence 1, App11	
13	410.5	11.6	3516	9 <td>US-10-152-661-257</td> <td>Sequence 257, App</td>	US-10-152-661-257	Sequence 257, App	
14	410.5	11.6	3516	9 <td>US-09-866-050A-257</td> <td>Sequence 257, App</td>	US-09-866-050A-257	Sequence 257, App	
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30	371	10.5	1931	12 <td>US-10-105-931-1</td> <td>Sequence 1, App11</td>	US-10-105-931-1	Sequence 1, App11	
31	371	10.5	2501	9 <td>US-09-981-397A-13</td> <td>Sequence 13, App1</td>	US-09-981-397A-13	Sequence 13, App1	
32	371	10.5	2709	10 <td>US-09-925-301-173</td> <td>Sequence 173, App</td>	US-09-925-301-173	Sequence 173, App	
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41	329.5	9.3	1428	9 <td>US-09-938-842A-882</td> <td>Sequence 882, App</td>	US-09-938-842A-882	Sequence 882, App	
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45	320.5	9.0	6383	9 <td>US-09-954-531-405</td> <td>Sequence 405, App</td>	US-09-954-531-405	Sequence 405, App	

ALIGNMENTS

RESULT 1
US-09-758-003-1
; Sequence 1, Application US/09758003
; Patent No. US20020098522A1
GENERAL INFORMATION:
APPLICANT: BAICHUAI, VIJAY R
HUNG, JIANING
HSU, HAILING
GOEDDEL, DAVID V
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
ASSAYS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758, 003
FILING DATE: 09-Jan-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/132,118
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T95-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2013
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-758-003-1

Alignment Scores:
Pred. No.: 0 Length: 2016
Score: 3545.00 Matches: 671
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-981-397a-16 (1-671) x US-09-758-003-1 (1-2016)

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Oy 481 ProGlyThrAlaGlyProArgValTyrPyrArgProLleProSerHisMetProSerLeu 500
Db 1441 CCAGGAACAGAGGCTCCAGAGTGTGTACAGGCCCAATTCGAAGTCATATCTTACTG 1500
Oy 501 HisAsnLleProValProGluThrAsnTyrLeuGluAsnThrProThrMetProPheSer 520
Db 1501 CATATATCCAGAGTCCGAGACACCACTATCTAGAAATTAACCCACCATGCTTACAG 1560
Oy 521 SerLeuProProThrAspGluSerLleLysTyrThrLleTyrAsnSerThrGlyLleGln 540
Db 1561 TCTTGGCCACCAAGATGATTAATAAATATACATATACATATAGTACTGATTCAG 1620
Oy 541 lleGlyAlaTyrAsnTyrMetGluLleGlyLysThrSerSerSerLeuLeuAspSerThr 560
Db 1621 ATTGGAGCTTACATTAATATGAGATGTGGAGCACTTATCATCACTAATAGACAGACA 1680

QY 561 AsnThrAsnPhenylsugluProAlaAlaLysTrpGlnAlaIlePheAspAsnThrThr 580
 |||||||
 Db 1681 AATAGCAACTTCAAGAAGACCAAGCTGCTAAGTACCAAGTATCTTGATTAATACCACT 1740
 |||||||
 QY 581 SerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTrpLysAsn 600
 |||||||
 Db 1741 AGCTGACGATTAACACCTGAGCCCAATCAGGGAATCTGGGAAAGCCACTGGAATAAAC 1800
 |||||||
 QY 601 CysAlaIlePheLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTrpGlu 620
 |||||||
 Db 1801 TGAGCCGTAACAGGCTTCCACACACTGCTCAGATTATGAAATTGACCATGACTATAGAG 1860
 |||||||
 QY 621 ArgAspLysLeuLysGluLysValTrpGlnMetLeuGlnLysTrpValMetArgGluGly 640
 |||||||
 Db 1861 CGAGATGACTGGAAGAAAGGTTTACCAGATGCTCAAAAGTGCTGATCAGGGAAGGC 1920
 |||||||
 QY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
 |||||||
 Db 1921 ATAAAGGAGCCACAGGTGGGGAAGCTGGCCAGGCGCTCCACAGTGTTCAGAGATCGAC 1980
 |||||||
 QY 661 LeuLeuSerSerLeuIleTrpValSerGlnAsn 671
 |||||||
 Db 1981 CTCTGAGCAGCTTGATTGATTCAGTCCAGCAAGAC 2013
 |||||||

RESULT 2

US-09-981-397A-15
 : Sequence 15, Application US/09981397A
 : Publication No. US20030082519A1
 : GENERAL INFORMATION:
 : APPLICANT: Axxima Pharmaceuticals AG
 : APPLICANT: Schubart, Daniel
 : APPLICANT: Habenberger, Peter
 : APPLICANT: Stein-Gerlach, Matthias
 : APPLICANT: Beyer, Dorian
 : TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
 : FILE OF INVENTION: Inhibition
 : FILE REFERENCE: AXM-004.1 US
 : CURRENT APPLICATION NUMBER: US/09/981,397A
 : PRIOR APPLICATION NUMBER: 2002-06-28
 : PRIOR FILING DATE: 2000-10-16
 : NUMBER OF SEQ ID NOS: 22
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 15
 : LENGTH: 2617
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (2141)..(2141)
 : OTHER INFORMATION: n = a,c,g or t
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (2311)..(2311)
 : OTHER INFORMATION: n = a,c,g or t
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (2452)..(2452)
 : OTHER INFORMATION: n = a,c,g or t
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (2496)..(2496)
 : OTHER INFORMATION: n = a,c,g or t
 : US-09-981-397A-15

Alignment Scores:

Pred. No.: 0
 Score: 3545.00
 Percent Similarity: 100.008
 Best Local Similarity: 100.008
 Query Match: 100.008
 DB: 9

Length: 2617
 Matches: 671
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-981-397A-16 (1-671) x US-09-981-397A-15 (1-2617)
 QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
 |||||||
 Db 1 ATGCACACAGACAGATGCTCTTGAATGATTAAGATGAATTCACATGACTTCTCGAGAGT 60
 |||||||
 QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisAspTrpGlnGly 40
 |||||||
 Db 61 GCAGAACTGCACAGCCGAGGCTTTGGAGAGTGTCTGTGTTTCCACAGAACCCAGCA 120
 |||||||
 QY 41 LeuMetLleGlyLysTrpValTrpLysGlyProAsnCysIleGluHisAsnGluAlaLeu 60
 |||||||
 Db 121 CTCATGATCATGAAGAACAGTGTACAGAGGCCCACTGATGAGCAGCAAGAGGCCCTC 180
 |||||||
 QY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuGly 80
 |||||||
 Db 181 TTGGAGAGAGCGAAGATGATCAACAGACTGAGACACAGCCGGGTGGAGGCTCTCC 240
 |||||||
 QY 81 ValIleIleGluGluGlyLysTrpSerLeuValMetGluTrpMetGluLysGlyAsnLeu 100
 |||||||
 Db 241 GTCATCATAGAGAGAGGAGTACTCCCTGGTATGAGATCATGAGAGGCAAGCCTG 300
 |||||||
 QY 101 MethHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleLeu 120
 |||||||
 Db 301 ATGCACGCTGCAGAAAGCCGAGATGATCTCCGCTTCTGTAAAGAGAGATATTG 360
 |||||||
 QY 121 GluIleIleGluGlyMetCysTrpLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
 |||||||
 Db 361 GAAATCATTTGAGAGAAATGCTGCTACTCATGCAAAAGCCGATACCAAGAGACTGAG 420
 |||||||
 QY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
 |||||||
 Db 421 CCTGAATAATCCCTGTGTGATTAATGACTTCCACTTAAGATCGCAGACCTCGGCTGGCC 480
 |||||||
 QY 161 SerPheLysMetTrpSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp 180
 |||||||
 Db 481 TCCTTTAAGATGTGAGCAAACTGATTAATGAAGACCAATGATGAGGAGGAGTGGAC 540
 |||||||
 QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTrpTrpMetAlaProGluHisLeuAsnAsp 200
 |||||||
 Db 541 GGCACCCCTAAGAAAGATGGCGGCACCCCTACTACTACATGGCGCCGAGACCTGAATGAC 600
 |||||||
 QY 201 ValAsnAlaLysProThrGlnLysSerAspValLysSerPheAlaValIleLeuTrpAla 220
 |||||||
 Db 601 GTCACCCCAAGCCCAAGAGAAAGTGGATGTGACAGCTTGTGTGATGACTCTGGGCG 660
 |||||||
 QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCys 240
 |||||||
 Db 661 ATATTTCGAATAGAGAGCCCATATGAATATCTATCTGTGAGCAGCAGTTCATATGTC 720
 |||||||
 QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTrpCysProArgGluIle 260
 |||||||
 Db 721 ATAAATCTGGGAAGAGCCAGATGCTGATGACATCACTGATGCTGCCCAAGAAAT 780
 |||||||
 QY 261 IleSerLeuMetLysLeuGlyTrpGluAlaAsnProGluAlaArgProThrPheProGly 280
 |||||||
 Db 781 ATCAGTCTCATGAAGCTCTGCTGGGAAGCGATCCGAGACCTGCGGACATTTCTGCGC 840
 |||||||
 QY 281 IleGluGluLysPheArgProPheTrpLeuSerGlnLeuGluGlnSerValGluAsp 300
 |||||||
 Db 841 ATTGAAGAAAAATTTAGGCTTTTATTTATTAAGTCAATTAGAGAAAGTGTAGAGAGAGC 900
 |||||||
 QY 301 ValLysSerLeuLysLysGluTrpSerAsnGluAsnAlaValValLysArgMetGlnSer 320
 |||||||
 Db 901 GTGAGAGATTAAAGAAAGAGTATTCAAGCAAAATGCAGTGTGAGAGATGCAGTCT 960
 |||||||
 QY 321 LeuGlnLeuAspCysValAlaIleAlaProSerSerArgSerAsnSerAlaThrGluGlnPro 340
 |||||||
 Db 961 CTTCACCTGATTTGTTGGAGATCACTTCAAGCCGCGCAATTCAGCCACAGAACACCTT 1020
 |||||||
 QY 341 GlySerLeuHisSerSerGlnGlyLeuGluMetGlyProValGluGlnSerTrpPheAla 360
 |||||||
 Db 1021 GGTTCACCTGCACAGTTCACAGGAGACTTGGGATGGGTCTGTGTGAGAGAGTCTCTGTTGCT 1080
 |||||||

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QY 361 ProSerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLeuGlnAsp 380
DB 1081 CTTTCCCTGGAGCACCACAGAGAAAGAGAGCCAGCTGACAGATTAACCTCAAGAC 1140
QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrGlyGlnGlnProArg 400
DB 1141 GAAGCCACTACATCTTTATGCGACCCGATGAGACAGACGAGAAACGACGCCAGCA 1200
QY 401 GlnAsnValAlaTyrAsnArgGluGluGluAlaArgArgValSerHisAspProPhe 420
DB 1201 CAGAAATGGCTTACACAGAGAGAGAGAAAGAGAGAGCGCTCCCTGACCTTTT 1260
QY 421 AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGlnGluGlyGlySerValTyrSer 440
DB 1261 GCACAGCAGACAGCTTACAGAGAAATTTTCAGAAATACAGAGAGAAAGCACTGTTATTC 1320
QY 441 SerAlaAlaSerHisGlnAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
DB 1321 AGTGCAGCCAGTCATGATGATGACAGCAGCAGCCCTCAGGCGCTCAGCCAGCAGCTCA 1380
QY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
DB 1381 GTACTGTATCAGAACATGATTAATATGATGCTCAGATGGCTTGGAAACAGACAGCTGGAT 1440
QY 481 ProGlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeu 500
DB 1441 CCAGGACAGCAGGCTCCAGAGCTTGGTACAGCCCAATTCAGATCATGCTAGTCTG 1500
QY 501 HisAsnIleProValProGlnThrAsnTyrLeuGlyAsnThrProThrMetProPheSer 520
DB 1501 CATATATTCAGCTGCTGAGACCAACTCTAGAGAAATACACCCAGCTGCTTACCTCAGC 1560
QY 521 SerLeuProProThrAspGlnSerIleLeuTyrThrIleTyrAsnSerThrGlyLeuGln 540
DB 1561 TCCTTGCACCAACAGATGAATCTATAAATATACATATACATATAGTCTGCAATTCAG 1620
QY 541 IleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThr 560
DB 1621 ATTGAGGCTCAATTAATATGAGATGAGATGGAGACAGTTCATCTACTACTACAGACACA 1680
QY 561 AsnThrAsnPheLeuGluGlnProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
DB 1681 AATAGCACTTCAAGAGAGAGAGCAGCTGCTAGTACCAAGCATCTTGTATTAATCCACT 1740
QY 581 SerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisThrPylAsn 600
DB 1741 AGTCGACGAGATAAACACCTGACCCCAATCAGGGAAATCTGGAAAGACACTGGAAAC 1800
QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGlu 620
DB 1801 TGTGCCCTTAAACTGGCTTACACAGTCTCAGATTGATGAATTAATGACCATCATATAG 1860
QY 621 ArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTyrValMetArgGlyLeu 640
DB 1861 CGAGATGAGACTGAAAGAAAGATTACAGATGCTCCAAAGTGGCTATAGAGGAAGGC 1920
QY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgGlyLeuAsp 660
DB 1921 ATTAAGGAGGAGCCAGGCTGGAGAGTGGCCAGGCGCTCCACAGTGTTCAGAGATCCAC 1980
QY 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
DB 1981 CTCTGAGCAGCTGATTTACGTACAGCCAGAAC 2013

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RESULT 3
US-09-854-133-676

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: Sequence 676, Application US/09854133
: Publication No. US20020183499A1
: GENERAL INFORMATION:
: APPLICANT: Lodes, Michael J.
: APPLICANT: Mohamath, Radooh
: APPLICANT: Henderson, Robert A.

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: APPLICANT: Benson, Darin R.
: APPLICANT: Secrist, Heather
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
: TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.475C10
: CURRENT APPLICATION NUMBER: US/09/854,133
: NUMBER OF SEQ ID NOS: 735
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 676
: LENGTH: 529
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-854-133-676

Alignment Scores:
Pred. No.: 1,14e-69 Length: 529
Score: 772.00 Matches: 169
Percent Similarity: 95.488 Conservative: 0
Best Local Similarity: 95.488 Mismatches: 5
Query Match: 21.788 Indels: 6
DB: Gaps: 0

US-09-981-397a-16 (1-671) x US-09-854-133-676 (1-529)

QY 274 AlaArgProThrPheProGlyIleGluGluLysPheArgProPheTyrLeuSerGlnLeu 293
DB 8 GCACGAGGACACATTTCTGCTGCAATGACAGAAATTTAGCCCTTTTATTAATGTCATATA 67
QY 294 GluGluSerValGluGluAspValLysSerLeuLysGlyLysTyrSerAsnGlu-AsnAl 313
DB 68 GAAGAAAGTGTAGAGAGAGAGAGCTGAAGAGTTTAAAGAAAGATTAATCAACGAAATATGC 127
QY 313 aValValLysArgMetGlnSerLeuGlnLeuAspGlyValAlaValProSerSerArgSe 333
DB 128 AGTTGTGAAGAGAAATGACATCTCTCA-CTTGAATTTGGGACATCTTCAAGCCGGTC 186
QY 333 rAsnSerAlaThrGluGlnProGlySer-LeuHisSerSerGlnGlyLeuGlyMetGlyP 353
DB 187 AATTCAGGCACAGAAAGAGCCGTGTTCACTTCCACAGTTCCAGGAGACTTGGATGGGTC 246
QY 353 rValGluGluSerTyrPheAlaProSerLeuGlnHisProGlnGluGluAsnGluProS 373
DB 247 CTGTGAGAGAGTCCCTGTTGCTCTCCCTGAGCACCACCAAGAAAGATGAGCCCA 306
QY 373 erLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHisLeuTyrGlySerArgMetAspA 393
DB 307 GCCTCAGAGTAAGTCCAGAGAGAGCCAC-TACCATCTTTATGCGACGCGCATGAGACA 365
QY 393 rGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArgGluGluGluArgArgA 413
DB 366 GGCAGACAGAAACAGCAGCCAGCAGAGATGCGTTTACACAGAGAGAGAGAGAAAGAGAC 425
QY 413 rGArgValSerHisAspProPheAlaGlnGlnArgProTyrGlu-AsnPheGlnAsnThr 432
DB 426 GCAGGCTCCCATGAGACCTTTTGACAGCAAAACCTTACGAGAAATTTTCAGAAATACA 485
QY 433 GluGlyLysGlyThrValTyrSerSerAlaIleSerHisGlyAsn 447
DB 486 GAGGAGAAAGCCCTGCT-TATTCAGTGCACAGCCAGTATGTTAAT 529

RESULT 4
US-09-918-995-17425
: Sequence 17425, Application US/09918995
: Publication No. US20030073623A1
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
: FILE REFERENCE: 20411-756
: CURRENT APPLICATION NUMBER: US/09/918,995
: CURRENT FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: US/09/235,076

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; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17425
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-17425

Alignment Scores:
Pred. No.: 176-56 Length: 392
Score: 641.00 Matches: 125
Percent Similarity: 96.92% Conservative: 1
Best Local Similarity: 96.15% Mismatches: 4
Query Match: 18.08% Indels: 0
DB: 9 Gaps: 0

US-09-981-397a-16 (1-671) x US-09-918-995-17425 (1-392)

QY 292 GlnleuglucjuserValGluGluaspValysSerleuLysGluTyfSerasnGlu 311
    |||||||  |||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 1 CAATTAGAGAGAAAGGATATAGAGACGTGAGCTTTTAAAGAAAGATATTCAACCAA 60

QY 312 AsnaIaValValysArqmetGlnSerleuGlnleuaspCyValAlaValProSerSer 331
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 61 AATCAGCTTGGAAGAGAAATGCACTCTTCACTTGATGTGGGGCAGTACCTTCAAGC 120

QY 332 ArgSerSnsrAlaThrGlnGlnProGlySerleuHisSerSerGlnGlyLeuGlyMet 351
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 121 CGGCAAAATTCAGCCACAGAACACCTGGTCACTGCACACCTCCAGGCACTTGGGATG 180

QY 352 GlyProValGluGluSerTrrPheAlaProSerleuGlnHisProGlnGluGluasnGlu 371
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 181 GGTCCTGTGGAGAGCTCCTGTGTCCTCTTCCCTGGAGCACCCACAGAAAGAGATGAG 240

QY 372 ProSerleuGlnSerLysleuGlnAspGluAlaAsnTyfHisleuTyfGlySerArqmet 391
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 241 CCCAGCCTGCAGATAACTCCAGAGAACCCAACTTATTATGCCAGCCGCGATG 300

QY 392 AspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyfAsnArgGluGluArg 411
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 301 GACAGGAGAGAGAAACAGACGCCACAGAGATGTGCTTACACAGAAAGAGGAAAG 360

QY 412 ArgArgValSerHisAspProPheAla 421
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 361 AGAGCGAGGCTCTCCATGACCTTTTGCA 390

RESULT 5
US-09-796-692-6140/C
; Sequence 6140, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077 001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
```

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; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6140
; LENGTH: 331
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-6140

Alignment Scores:
Pred. No.: 431e-46 Length: 331
Score: 538.00 Matches: 102
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.18% Indels: 0
DB: 9 Gaps: 0

US-09-981-397a-16 (1-671) x US-09-796-692-6140 (1-331)

QY 570 AlaySTyrglnAlaIlePheaspAsnThrSerleuThrAspLysHisleuAspPro 589
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 329 GCTAGATGCCAAGCATATCTTTGATAATATACCACTAGTGCAGCGATTAACACTGGACCCA 270

QY 590 IleArgGluAsnleuGlyLysHisTrpLysAsnCysAlaArgLysleuGlyPheThrGln 609
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 269 ATCAGGGAAATCTGGGGAACACTGGAAGAAACTGCTCAACTGCGCTTCAACAG 210

QY 610 SerGlnIleAspGluIleAspHisAspTyfGluArgAspGlyLeuLysGluLysValTyf 629
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 209 TCTCAGATTGATGAATGACCATGACTATAGCGAGTGGAGTGAAGAGAAAGGTTTAC 150

QY 630 GlnMetleuGlnLysTrpValMetArgGluGlyLysGlyAlaThrValGlyLysleu 649
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 149 CAGATGCTCCAAAGTGGGTGATGAGGAGCAATAAAGGAGCCAGCGTGGGAGCTG 90

QY 650 AlaGlnAlaLeuHisGlnCysSerArgIleAspLeuLeuSerSerleuIleTyfValSer 669
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 89 GCCCAGGCGCTCCACACAGTGTCCAGATCGACCTTGGACGACCTGATTACGTACGC 30

QY 670 GlnAsn 671
    |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 29 CAGAAC 24

RESULT 6
US-10-040-862-6140/C
; Sequence 6140, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
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; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6140
; LENGTH: 331
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-6140

Alignment Scores:
Pred. No.: 4,31e-46 Length: 331
Score: 538.00 Matches: 102
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.18% Indels: 0
Gaps: 0
DB: 9

US-09-981-397a-16 (1-671) x US-10-040-862-6140 (1-331)

QY 570 AAlaSYrGlnAlaIlePheAspAsnThrThrSerLeuThrAspLysHisLeuAspPro 589
DB 329 GCTAAGTACCAAGCATCTTTGATATATACCACTAGCTGACGATTAACACCTGGACCCA 270
QY 550 lIeaRgLuAsnLeuGlyLysHisTrpLysAsnCysAlaArGlyLeuGlyPheThrGln 609
DB 269 ATCAGGAAAAATCTGGAAAGCAGCAGTGAAGAAACCTGCCCTGAACCTGGCTTACACAG 210
QY 610 SerGlnIleAspGluIleAspHisAspTyrGluArGAspGlyLeuLysGluLysValTyr 629
DB 209 TCTCGATTGATGAATAATTGACCATGATGAGCGAGATGAGACTGAAGAAAGCTTAC 150
QY 630 GlnMetLeuGlnLysTrpValMetArgGluGlyIleLysGlyAlaThrValGlyLysLeu 649
DB 149 CAGATGCTCCCAAAAGTGGGTATGAGGAGCAATAAAGGAGCCAGGTGGGAGAGCTG 90
QY 650 AlaGlnAlaLeuHisGlnCysSerArgIleAspLeuLeuSerSerLeuIleTyrValSer 669
DB 89 CCCCAGCGCTCCACACAGTGTCCAGATCGACCTTCTGAGAGCTTGAATTAGCTCAGC 30
QY 670 GlnAsn 671
DB 29 CAGAAC 24

RESULT 7
US-09-879-536-495
; Sequence 495, Application US/09879536
; Patent No. US20020144298A1
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
```

```

; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dertl, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/879,536
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/088,801
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 495
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(606)
; OTHER INFORMATION: n = A,T,C or G
US-09-879-536-495

Alignment Scores:
Pred. No.: 5,71e-44 Length: 606
Score: 521.00 Matches: 99
Percent Similarity: 99.00% Conservative: 0
Best Local Similarity: 99.00% Mismatches: 1
Query Match: 14.70% Indels: 0
Gaps: 0
DB: 10

US-09-981-397a-16 (1-671) x US-09-879-536-495 (1-606)

QY 572 TyrGlnAlaIlePheAspAsnThrThrSerLeuThrAspLysHisLeuAspProIleArg 591
DB 3 TACCAAGCATCTTTGATATATACCACTAGCTGACGATTAACACCTGGACCATTCAGC 62
QY 592 GlnAsnLeuGlyLysHisTrpLysAsnCysAlaArGlyLeuGlyPheThrGlnSerGln 611
DB 63 GAAATCTGGGAAACACACGAAACAACTGCCCTGAACCTGGCTTACACAGCTCAG 122
QY 612 lIeaSpGluIleAspHisAspTyrGluArGAspGlyLeuLysGluLysValTyrGlnMet 631
DB 123 ATTGATGAATTTGACCATGACTATGAGCGAGATGAGTGAAGAAAGGATTACCGAGATG 182
QY 632 LeuGlnLysTrpValMetArgGluGlyIleLysGlyAlaThrValGlyLysLeuAlaGln 651
DB 183 CTCCAAAAGTGGGTATGAGGAGCAATAAAGGAGCCAGCGTGGGAGAGCTGGCCAG 242
QY 652 AlaLeuHisGlnCysSerArgIleAspLeuLeuSerSerLeuIleTyrValSerGlnAsn 671
DB 243 GCGCTCCACACAGTGTCTCTGATCGACCTTCTGACACAGCTTGAATTAGCTCAGCCAGAC 302

RESULT 8
US-09-960-352-4340
; Sequence 4340, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nenping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511, 006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4340
; LENGTH: 430
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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 19-LIB3057-015-Q1-K1-E11
US-09-960-352-4340

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Alignment Scores:
Pred. No.: 2,86e-38 Length: 430
Score: 463.00 Matches: 92
Percent Similarity: 71.72% Conservative: 12
Best Local Similarity: 63.45% Mismatches: 39
Query Match: 13.06% Indels: 2
DB: 10 Gaps: 1,

```

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US-09-981-397a-16 (1-671) x US-09-960-352-4340 (1-430)
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OY 423 GlnAproThrgluAsnPhenGlnAsnThrGluGlySerGlyThrValTyrSerSerAla 442
DB 1 CAGAGACCTTATGAGTCTGCTCAGAGCCAGGATTAAGCCCTGCTTACCTGCTGCTG 60
OY 443 AlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeu 462
DB 61 ATGAGTCACACAGGTGAGCCAGCAGCCAGCGGGCTTAAGCACCACCCAGTCACCA 120
OY 463 TyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGly 482
DB 121 TACTGGAGAGATGGA-----TCATTTCATCCGCTTGAGTGAAGCCGCTGAGACCTGGG 174
OY 483 ThrAlaGlyProAlaValTyrTyrArgProIleProSerHisMetProSerLeuHisAsn 502
DB 175 ACCATGAGTCACAGAGTTTGATAGGGCCAAACCCAGCCAGCCAGCCATGCTATATAA 234
OY 503 IleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeu 522
DB 235 ACATCAGTCCCTGAGACACCTCCTGGGAGACACCCACCATTCATTCACCTCCTTG 294
OY 523 ProProThrAspGluSerIleLeuTyrThrIleTyrAsnSerThrGlyIleGlnIleGly 542
DB 295 CCATTCAGAGATGAGTCTTCAAAATATACCATACACAGCATCTCTGCAATTCAGATTGGC 354
OY 543 AlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThrAsnThr 562
DB 355 GACAGTATATTCATGGAGATTGGTGGATGATGATTCATGCTGCTGACACACATACATG 414
OY 563 AsnPhelysGluGlu 567
DB 415 AACCTGAAGAAGAG 429

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RESULT 9

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US-10-198-846-13921
; Sequence 13921, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steilmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198, 846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306, 220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ. ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13921
; LENGTH: 2111

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931,

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; LOCATION: 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941,
; LOCATION: 1942, 1943, 1944, 1945, 1946, 1947, 1948, 2007, 2096, 2110,
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13921

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Alignment Scores:
Pred. No.: 1.83e-35 Length: 2111
Score: 445.50 Matches: 152
Percent Similarity: 42.59% Conservative: 101
Best Local Similarity: 25.59% Mismatches: 187
Query Match: 12.57% Indels: 155
DB: 9 Gaps: 22

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US-09-981-397a-16 (1-671) x US-10-198-846-13921 (1-2111)
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```

OY 1 MetGlnProAspMetSerLeuAsnValIleLys----- 11
DB 156 CTGGCACCTTCCAGCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 215
OY 12 MetLysSerSerAspPheLeuGluSerAlaGluLeu---AspSerGlyGlyPheGlyLys 30
DB 216 TTGGTGTCATCGAGAGCTGAGAACAGGAGCTGCTGGCAAAAGCGGGTTCGGCACA 275
OY 31 ValSerLeuGlySerPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGly 50
DB 276 GTGTTCCGGGGCGCACATAGGAAGTGGGC-----TACGATGTG 314
OY 51 ProAsnGlyIleGluHisAsnGluAlaLeuGluGluAlaLysMetMetAsnArgLeu 70
DB 315 GCGGTCAAGATCGTAACCTGGAAGCGATATCCAGGAGGTCAAGGCCCATGCGCAAGCTCG 374
OY 71 ArgHisSerArgValValLysLeuLeuGlyValIle-----IleGluGlu 85
DB 375 GATACGCAATTCGTCGCGCCTTAGAAGGGATTATCAGAAAGTGAACCTGGACCAAGAT 434
OY 86 GlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeuLys 105
DB 435 CCCAGCGGGCTGCTGGTGACTAATTCATGAGAGAGGCTCTTGTGGGGCTGCTGACG 494
OY 106 AlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeuGluIleIleGluGly 125
DB 495 TCCACAGTCCCTGCGCCCTGCGCTCTTGGCGCTGGAAGAGTGGTCTGGG 554
OY 126 MetCysTyrLeuHisGlyLysGly-----ValIleHisLysAspLeuLysProGluAsn 143
DB 555 ATGTTTACTCTGACGACGACGACGACGACGCTCTCTGCGCGGACCTCAAGCCATCCAC 614
OY 144 IleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPheLys 163
DB 615 GTCTCTGTGACCCACAGAGCTGACGTCGACGTCGACGATTTGGCTGCTCACATTTTCAG 674
OY 164 MetTyrSerLysLeuAsnAsnGluGluHisAsnGluLeuArgLeuValAspGlyThrAla 183
DB 675 GGAAGCTCACAG-----TCAGGACACAGCG 658
OY 184 Lys---LysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspValAsn 202
DB 699 TCCGGGAGCGCAGGGGCGCCCTGCGCTACTTGGCCCAAGAACTGTTTGTTAACGTAAC 758
OY 203 AlaLysProThrGluLysSerAspValTyrSerPheAlaValLeuTyrPalaIlePhe 222
DB 759 CGAAGGCTCCACACAGCAGTACAGTACAGCTTGGGATTCCTAATGTGGCAGTCTT 818
OY 223 AlaAsnLysGlu-----ProTyrGlu-----AsnAlaIleCysGlu 234
DB 819 GCTGGAAGAGAGATTGAGTTGCCAACGACCAATCACTGCTGACAGCAGTGTGCAAC 878
OY 235 GlnGluLeuIleMetCysIleLysSerGlyAsnArgProAspValAspIleThrGlu 254
DB 879 AGGCAG-----ACCGGCGCTTCATTTGGCTGAGTGGCCCAA 914
OY 255 TyrCysProArgGlu-----IleIleSerLeuMetLysLeuCysTrpGlu 269

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Db      915 GCCGGCCCTGAGACTCCGGCTTACAGAGCAGTAACTCAGCTCTGAGACC 974
QY      270 AlaAsnProGluAlaArgProThrPhe-----ProGlyIleGluIuLysPhe 285
Db      975 AGTGAGCCCAAGACAGACCTCTTCCAGAAATCCCTAACAAATGATGATGCTTC 1034
QY      286 ArgProPheTyrLeuSerGlnLeuGluIuSerValGluIuAspValLysSerLeuLys 305
Db      1035 CAG-----ATGGTGAGAACATATGATGCTGCGCTCTCCACGGTAAG 1079
QY      306 LysGluTyrSerAsnGluAsnAlaValLysArgMetGlnSerLeuGlnLeuAspCys 325
Db      1080 GATTTCCTGTCACCTCAGAGCAGCAATAGACATTT----- 1118
QY      326 ValAlaValProSerSerArgSerAsnSerAlaThrGluGlnProGlySerLeuHis 345
Db      1119 ---TCTATCCAGACTCA----- 1133
QY      346 SerGlnGlyLeuGlyMetGlyProValGluIuSerTyrPheAlaProSerLeuHis 365
Db      1134 -----GGCCAGAGGAGGAGCAAGAAATGATGGCTTACAGAAACCATACAAAC 1181
QY      366 ProGlnGluIuAsnGlnProSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHis 385
Db      1182 CAGCACTCTCTTAATGATCATGCTTCTCAGTGGCTA----- 1220
QY      386 LeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyr 405
Db      1221 -----AACAACTGAATCTAGAGGAGCCTCCAGCTCTGTT----- 1256
QY      406 AsnArgGluGluGluArgArgArgValSerHisAspProPheAlaGlnIuAsnArgPro 425
Db      1257 -----CCTAA-AAATGCCAGACT 1276
QY      426 TyrGluAsnPheGlnAsnThrGluIuLysGlyThrValTyrSer-SerAlaAlaSerHis 445
Db      1277 TACCAGAGGAGGAGGAGCAGAGAGAGGTTCCAGAACGCTGAGCAGCAGCAGCATC 1336
QY      445 sGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAs 465
Db      1337 TTCAGATTCGATGCCCAACT-----CCCCAGACTCCAGAGACCTCACTTTCAG 1387
QY      465 nasnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAlaG1 485
Db      1388 AAACCAATGCCCACT-----CCTACCTCAACGAGAAC----- 1421
QY      485 yProArgValTrrPyrArgProIleProSerHisMetProSerLeuHisAsnIleProVa 505
Db      1422 -----CCAACT-----CCTGG 1432
QY      505 lProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerLeuProThr 525
Db      1433 ACCCGAGGAGGAGGAGGAGGAGGAGCAGACAGACAGCATGCTGCTGAGAGACCCCGGA 1492
QY      525 rAspGluSerIleLys-----TyrThrIleTyrAsnSerThrGlyIleGlnI1 541
Db      1493 GCCAATCCAGTAACAGGCGCACCGCTGTAACATATACAACTGCTGGGGTCCAGT 1552
QY      541 eGlyAlaTyrAsnTyrMetGluIleGlyLysThrSerSer 554
Db      1553 TGGAGACAACAACACTACTGACTATGCACAGACACTGCC 1592

```

RESULT 10

```

US-09-862-027-7
; Sequence 7, Application US/09862027
; Patent No. US2002014248A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. US2002014248A1el Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862.027
; CURRENT FILING DATE: 2001-05-21

```

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; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1697
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(1492)
US-09-862-027-7

Alignment Scores:
Pred. No.: 4,82e-35
Score: 440.00
Percent Similarity: 42.86%
Best Local Similarity: 26.10%
Query Match: 12.41%
DB: 10
Gaps: 21

US-09-981-397A-16 (1-671) x US-09-862-027-7 (1-1697)

QY      19 GluSerAlaGluLeu---AspSerGlyGlyPheGlyLysValSerLeuCysPheHisArg 37
Db      2 GAGAACCAAGAGACTCTGCGCAAGAGCGGGTTCCGACAGTGTTCGGGCGCAACATAGG 61
QY      38 ThrGlnGlyLeuMetIleMetLysThrValTyrLysGlyProAsnGlyIleGluHisAsn 57
Db      62 AAGTGGGCG-----TACGATGTGGCGGTCACATGCTAAACATCG 100
QY      58 GluAlaLeuLeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLys 77
Db      101 AAGCGGATATCCAGGAGAGTCAAGGCCATGCAATGATGATAGCAATTCGTCTGCGC 160
QY      78 LeuLeuGlyValIle-----IleGluGluGlyLysTyrSerLeuValMet 92
Db      161 CTAGAAAGGGGTATTCAGAGAGGTGAATGGAGCAATCCCAAGCCGCTGTGCTGACT 220
QY      93 GluTyrMetGluLysGlyAsnLeuMetHisValLeuLysAlaGluMetSerThrProLeu 112
Db      221 AATTCATGAGAACAGCGCTCTTGGCGCTTGGCGCTGCGCACTGCGCTGCGCTGCG 280
QY      113 SerValLysGlyArgIleIleLeuGluIleIleGluGlyMetCysTyrLeuHisGlyLys 132
Db      281 CCGCTCCCTTGGCGCTGCTGTAAGAGATGGGCTGGAGTGTATTACTGACAGACAG 340
QY      133 Gly-----ValIleHisLysAspLeuLysProGluAsnIleLeuValAspAsnAspPhe 150
Db      341 AACCGGTGCTCTGACCGGAGCTCAAGCCATCAACGCTGCTGAGACCCAGACTG 400
QY      151 HisIleLysIleAlaAspLeuGlyLeuAlaSerPheLysMetTrrPserLysLeuAsnAsn 170
Db      401 CACGTCAAGCTGGCGAGATTGCTGCTGCAATTTCAGAGAGCTCACAG----- 451
QY      171 GluGluHisAsnGluLeuArgGluValAspGlyThrAlaLys---LysAsnGlyGlyThr 189
Db      452 -----TCAGGAGAACGGTCCGGGAGACCGAGGGGCGAC 484
QY      190 LeuTyrTyrMetAlaProGluHisLeuAsnAspValAsnAlaLysProThrGluLysSer 209
Db      485 CTGGGCTACTTGGCCCGCAAGACTGTTGTTAACGTAAACCGGAAGGCTCCACAGCGCT 544
QY      210 AspValTyrSerPheAlaValAlaLeuThrAlaIlePheAlaAsnLysGlu----- 226
Db      545 GAGCTCTACAGCTTCGGGATCTTAATGTGGCAGAGCTTGTGGAGAGAGATTGAGTTG 604
QY      227 ProTyrGlu-----AsnAlaIleCysGluGlnGlnIleMetCysAlle 241
Db      605 CCAACCGAACCATCTGCTGTAGACAGACGTGCAACAGGACAG----- 649
QY      242 LysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGlu----- 259

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Db 650 -----AACGGGCTTATTGGCTGAGCTGCCCCAACCGGGGCTTGAGACTCCCGGC 700
QY 260 -----IleIleSerMetLysLeuGlyTyrPheValAsnProGluAlaArgPro 276
Db 701 TTGAGAGAGCTGAAGAGCTAATGACGCTGCTGGAGCAGTGAAGCCCAAGACAGACGCC 760
QY 277 ThrPhe-----ProGlyIleGluGlnLysPheArgProPheTyrLeuSerGln 292
Db 761 TCCCTCCAGGAATGCCCTACCAAAACGATGAAGATCTTCCAG-----ATG 805
QY 293 LeuGluGlnSerValGluGlnAspValLysSerLeuLysGluTyrSerAsnGluAsn 312
Db 806 GTGGAGACACATATGAATGCTGCTGTCTCCACGCTAAGGATTTCTGCTCAGCTCAGC 865
QY 313 AlavalValLysArgMetGlnSerLeuGlnLeuAspValAlaValProSerSerArg 332
Db 866 AGCAGCAATGAGAGATT-----TCTATCCAGAGTCA--- 898
QY 333 SerAsnSerAlaThrGlnProGlySerLeuHisSerSerGlnGlyLeuGlyMetGly 352
Db 899 -----GGCCCAAGA 907
QY 353 ProValGluGlnSerTrpPheAlaProSerLeuGlnHisProGlnGlnGluAsnGluPro 372
Db 908 GGGACAGAAAATGATGGCTTTAGCAGAACCATAGAAAACAGACACTCTGTAATGATGTC 967
QY 373 SerLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHisLeuTyrGlySerArgMetAsp 392
Db 968 ATGGTTTCTGAGTGGCA-----AAC 988
QY 393 ArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArgGluGlnGluArg 412
Db 989 AAACGTCAATGATAGAGGCTCCAGCTGTGT----- 1021
QY 413 ArgArgValSerHisAspProPheAlaGlnGlnArgProTyrGluAsnProGlnAsnThr 432
Db 1022 -----CCTAA-AAATGCCCGAGCTTACCAAGAGGAGGACAGGACCA 1062
QY 433 GluGlyLysGlyThrValTyrSer-SerAlaAlaSerHisGlyAsnAlaValHisGlnPro 452
Db 1063 AGAGAGACAGCTTCCACACCCCTGGACAGCAGCAGCATCTTCAGATTGCGTCCAGC 1122
QY 452 OSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHis 472
Db 1123 T-----CCCCAGACTCCAGACCTCAACTTTCAGAAACAGATGCCAC----- 1168
QY 472 SGIYPhneglyThrArgProLeuAspProGlyThrAlaGlyProArgValIrrPtyrArgPr 492
Db 1169 -----CCTACCTCAACTGGAACA----- 1186
QY 492 oIleProSerHisMetProSerLeuHisAsnIleProValProGluThrAsnTyrLeuGln 512
Db 1187 -----CCAGT-----CCTGGACCCCGAGGGAATCAGGGGCG 1218
QY 512 yAsnThrProThrMetProPheSerSerLeuProProThrAspLysSerLeuLys----- 530
Db 1219 TGAGAGACAGAGCATGATGCTGTCGACAGACCCGAGCCCAATCAGTAACAGGGCG 1278
QY 531 -----TyrThrIleLysAsnSerThrGlyIleGlnIleGlyAlaTyrAsnTyrMetGln 548
Db 1279 ACCGCTCGTTACATATACAACTGCTGGGTGCAAGTGGAGACAAACAACACTTGAC 1338
QY 548 uIleGlyGlyThrSerSer 554
Db 1339 TATGCAACAGACAACTGCC 1357

```

RESULT 11
US-10-164-080-1

; Sequence 1, Application US/10164080
; Publication No. US20030087411A1

; GENERAL INFORMATION:

; APPLICANT: BIRD, Timothy, A.
; APPLICANT: HOLLAND, Pamela, M.

```

; APPLICANT: PESCHON, Jacques, J.
; APPLICANT: VIRCA, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKRYIN REPEATS (DAKAR) AND
; FILE OF INVENTION: USE
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,959
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(2367)
; OTHER INFORMATION:
US-10-164-080-1

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```

Alignment Scores:
Pred. No.: 8.09e-32 Length: 2370
Score: 410.50 Matches: 164
Percent Similarity: 43.43% Conservative: 84
Best Local Similarity: 28.72% Mismatches: 209
Query Match: 11.58% Indels: 116
Gaps: 25

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US-09-981-397a-16 (1-671) x US-10-164-080-1 (1-2370)

```

QY 14 SerSerAspPheLeuGlnSerAlaGlnLeuAspSerGlyIlePheGlyLysValSerLeu 33
Db 64 GCGCGCAATTCGAGGCTGGAGAGAGTGGCTCGGCGCGCTTCGCGGCAAGTACAG 123
QY 34 CysPheHisArgThrGlnGlyLeuMetIleMetLysThr-----ValTyrLysGly 50
Db 124 GTGGCGCAT-----GTGCACTGGAAGACGTGGCTCGGATCAAGTCTCG 168
QY 51 ProAsnGly-----IleGlnHisAsnGlu-----AlaLeuGlnGlnAlaLysMetMet 67
Db 169 CCAGTCTGACGTCGACGACAGCAGAGAGATGAGAGCTCTGGAGAGAGTAAAGATG 228
QY 68 AsnArgLeuArgHisSerArgValValLysLeuLeuGlnValIleIleGluGluGlyLys 87
Db 229 GAGATGGCAAGTCCGATACATTCCTGCTACGCGCATATGCCAGAA-----CCT 282
QY 88 TyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeuLysAlaGlu 107
Db 283 GTGGCTTGGTGCATGAGGATGATGACAGACAGGCTCCCTGAGAAAGCTGCTGACAG 342
QY 108 MetSerThrProLeuSerValLysGlyArgIleIleLeuGlnIleIleGluGlyMetCys 127
Db 343 -----CCATTGGCTTGGAGCTGGCGTTCGATGTCAGACAGACAGCCGTCGATGAC 399
QY 128 TyrLeuHis-----GlyLysGlyValIleHisLysAspLeuLysProGluAsnIleLeu 145
Db 400 TTCTGATTCGATGATGCTCCGCACTGCTCACCCTAGACCTGAAGCCAGGACATCTCTG 459
QY 146 ValAspAsnAspPheHisIleLysIleAlaAspLeuGlnLeuAlaSerPheLysMetTrp 165
Db 460 CTGGATGCCACATACATGTCATGCAAGATTTGACTTTGGGCTGGCC----- 504
QY 166 SerLysLeuAsnAsnGlnGlnHisAsnGlnLeuArgIleValAspGlyThrAlaLysLys 185
Db 505 ---AAGTCAATAGGCAATGCCACTCTCAGACCTCAGATGATGATGCGCTTT----- 555
QY 186 AsnGlyGlyThrLeuTyrTyrMetAlaProGlnHisLeuAsnAspValAsnAlaLysPro 205
Db 556 -----GGTACAAATCGCTTACCTCCCTCCAGAGAGGAATTCGTAGAGAGACCCCTTGT 609

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Db 556 -----GGTACAAATGCTTACCTCCCTCCAGAGCAATTCGTGAGAAAGCGCTTGT
Oy 206 ThrGluysSerAspValTyrSerPheAlaValLeuTTPalaIllePheAlaSerLys 225
Db 610 GACACCAACATGATGTATACAGCTTGCGCATGTGATGCTGGGTCTTACACAGAG 669
Oy 226 GluProTyrGluAsnAlaIlleCysGluGlnGlnLeuIleMetCysIlleLysSerGlyAsn 245
Db 670 AAGCATTTGGAGATGAAGAAGACATCTTACACATCATGATGAAGTGGTAAAGGCGCAC 729
Oy 246 ArgProAspValAspAspIleTherGluTyrCysProArg-----GluIleLysSer 262
Db 730 CGCCAGAGCTGCACACCATCTGCAGACCCCGCGCGCTGCTGTCAGAGCTGATAGG 789
Oy 263 LeuMetLysLeuCysTyrProlAlaAsnProGluAlaArgProTherPheProGlyIleGlu 282
Db 790 CTCATGCAACGGTGTGTCATGCAAGACCCACAGAGTGGCGCCACTTCCAGAAATTTACC 849
Oy 283 GluLysPheArgProPheTyrLeuSerGlnLeuGlnGlnSerValGluGluAspValLys 302
Db 850 TCTGAA-----ACAGAAAGACCTTTGTGTGAGAACCCCTGATGAGAGAGTGA 894
Oy 303 SerLeuLysLysGluTyrSerAsnGluAsnAlaValLysArgMetGlnSerLeuGln 322
Db 895 GACCTGGCTCATGAGCCAGCGAGAAAGC-----TCTCTAGAG 933
Oy 323 LeuAspCysValAlaValPro---SerSerArgSerAsnSerAlaTherGluInProGly 341
Db 934 TCCAGAGAGTGAAGGCGCGAGCTTCACGCTCAAGCGCGCTGCTCCGCCCTTC 993
Oy 342 SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGlnGlnSerTyrPheAlaPro 361
Db 994 GATAACGACTGCAGCTCTCCGAGTGTCTGCACAGTTG---GACTCTGGGATCCAG 1050
Oy 362 SerLeuGluHisProGlnGlnGluAsnGluProSerLeuGlnSerLeu---GlnAsp 380
Db 1051 ACTCTTGAAAGCGCCGAGAGAGCTCAGCCGAGATTCTCTGATGACAGCTCCATCGACC 1110
Oy 381 GluAlaAsnTyrHisLeuTyrGly---SerArgMetAspArgGlnTherLysGlnInPro 399
Db 1111 AGCAGTGGCAAGAGGCTCTCGGGGTCTCTCAGTGTGACTAGCCTTTTCTCCAGAGA 1170
Oy 400 ArgGlnAsnValAlaTyrAsnArgGluGlnGluAlaGlyArgArgValSerHisAspPro 419
Db 1171 TCGCTGTACATGCTCTTTGAGCGGAGAGCTTC-AAACAGGCGA-----CCT 1214
Oy 420 PheAlaGlnGlnArgProTyrGluAsnPheGlnAsnTherGlnGlyLysGlyTherValTyr 439
Db 1215 GGGCCCCACAGACATCCAGAGAA-----GAAGCTAGTGGATGCCATCAT 1259
Oy 440 SerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSer-----GlyLeu 455
Db 1260 -----ATCAGGGGAGACACCACAGCGCTGATGAGATCTTCAAGCCCAAGATGTGACTT 1313
Oy 456 ThrSer----- 457
Db 1314 GGTCTTAGACACAGCAGTGCACCTGCTGCTGCTGAGAGCGGAGAGAGAGAGT 1373
Oy 458 -----GlnProGlnValLeuTyrGlnAsnAsnGlyLeu 468
Db 1374 TGTCAGTGGCTGTGTTAACAAATGCCAACCCCAACT---GACCACACAGAAAGCGCTC 1430
Oy 469 Tyr---SerSerHisGlyPheGlyThr----- 476
Db 1431 TACACCACTGCATATGCTGTGAGCCGAGAGAGAGAGTGAATTTGAGAGTACTGCTAGC 1490
Oy 477 -----ArgProLeuAsp---ProGlyTherAlaGlyP 486
Db 1491 CCGAGAGACAGCTGTCAATGCCAAGAGATGAAGACACAGTGGAGTGGCTTGGCAGC 1550
Oy 486 TGAATGValTyrTyrArgProIleProSerHisMetProSerLeuHisAlleProValP 506

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Db 1551 CCAGAAATGGGATGAGGCCACACAGGCTG-CTGCTAGAG---AAGAACTCTTCTGTCA 1606
Oy 506 roGluThrAsnTyrLeuGlyAsnThPro 515
Db 1607 ATGAGGTGACTTTGAGGGCGGAAACACCC 1635

RESULT 13
US-10-152-661-257
; Sequence 257, Application US/10152661
; Publication No. US20030022835A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c5
; CURRENT APPLICATION NUMBER: US/10/152,661
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/866,050
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/221,232
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/206,650
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/312,283
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00051
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 09/188,930
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: 09/069,726
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 3516
; TYPE: DNA
; ORGANISM: Mouse
US-10-152-661-257

Alignment Scores:
Pred. No.: 1,456-31 Length: 3516
Score: 410.50 Matches: 164
Percent Similarity: 43.43% Conservative: 84
Best Local Similarity: 28.72% Mismatches: 209
Query Match: 11.58% Indels: 116
Gaps: 25

US-09-981-397A-16 (1-671) x US-10-152-661-257 (1-3516)
Oy 14 SerSerAspPheLeuGluSerAlaGluAspSerGlyGlyPheGlyLysValSerLeu 33
Db 58 GCGGCGCAATTCGACAGGCTGGGAGAGGTGGGCTGGGCGGCTTGCGGAGGTACAG 117
Oy 34 CysPheHisArgThrGlnGlyLeuMetIleMetLysThr-----ValTyrLysGly 50
Db 118 GTGGCGCAT-----GTGCACGTGAAAGAGCTGGCTGGCATCAAGTGCCTG 162
Oy 51 ProAsnCys---LleGluHisAsnGlu-----AlaLeuLeuGluGluAlaLysMetMet 67
Db 163 CCCAGTCTGCAGCTGCGAGACAGGCAAGTGAAGTCCCTGAGAGAGTGAAGATG 222
Oy 68 AsnArgLeuArgHisSerArgValValLysLeuLeuGlyValIleLleGluGluGlyLys 87
Db 223 GAGATGCCCAAGTCCGATACATTTCTGCTGTGACGATATGCGAAGAA-----CCT 276
Oy 88 TyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeuLysAlaGlu 107
Db 277 GTGGGCTTGTGTCATGAGTACATGAGACAGAGGCTCCCTGAGAGAGCTGCTGGCTCAGAG 336

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OY 108 MetSerThrProLeuSerValLysGlyArgIleIleLeuGluIleIleGluLysMetCys 127
Db 337 ---CCATTGCCCTTGGGAGCTGGCGTTTGGCATCTGCACAGACAGACCCGTGGCATGAAC 393
OY 128 TyrLeuHis-----GlyLysGlyValIleHisLysAspLeuLysProGluAsnIleLeu 145
Db 394 TTCCGTCATTGCATGCTCTCCGCCACTGCCTAGACCTGAAAGCCAGCAACATCTCTG 453
OY 146 ValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPheLysMetTrp 165
Db 454 CTGGATGCCCACTACCATGCTCAAGATTCTTGACTTTGGCTGGC----- 498
OY 166 SerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAlaSpGlyThrAlaLys 185
Db 499 ---AAGTGCATGGCATGCTCCCATCTCATGACCTCAGCATGATGGCTGTT----- 549
OY 186 AsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLysAsnAspValAlaAsnIlePro 205
Db 550 -----GGTACATGCTTACCTCCCTCCAGAGCAATCTCGAAGACAGCGCTTGT 603
OY 206 ThrGluLysSerAspValTyrSerPheAlaValIleLeuTrpAlaIlePheAlaAsnLys 225
Db 604 GACACCAACATGATGTTATACAGCTTGCCATTGTGATCTGGGTGCTTAACACAGAG 663
OY 226 GluProTyrGluAsnAlaIleCysGluGluGluLeuIleMetCysIleLysSerGlyAsn 245
Db 664 AAGCATTTGCAGATGAAGAAAGAACATCTACACATCATGATGAAGTGAAGGCCAC 723
OY 246 ArgProAspValAlaAspIleThrGluTyrCysProArg-----GluIleLeuSer 262
Db 724 CGCCGAGCGCCACCCATCTGCAGACCCGCGCGTGCCTGTCCAGCCTGATGAGG 783
OY 263 LeuMetLysLeuCysTyrGluAlaAsnProGluAlaIleValProThrPheProGlyIleGlu 282
Db 784 CTCATGACACGCTGTGTCATGCACACCCACAGCGCGCCACCTTCCAGAAATTAAC 843
OY 283 GluLysPheArgProPheTyrLeuSerGluLeuGluLysSerValGluLysAspValLys 302
Db 844 TCTGAA-----ACAGAAAGACCTTTGTGAGAGCCCTGATGAGAGAGGTGA 888
OY 303 SerLeuLysGluTyrSerAsnGluAsnAlaValIleLysArgMetGluSerLeuGln 322
Db 889 GACCTGGCTCATGAGCCAGCGGAGAAAG-----TCTCTAGAG 927
OY 323 LeuAspCysValAlaValPro---SerSerArgSerAsnSerAlaThrGluGlnProGly 341
Db 928 TCCAAGATGAGGCCAGGCCGAGTCTCAGCCTCAAGCGGCTCTGCTCCCTTC 987
OY 342 SerLeuHisSerSerGluGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaPro 361
Db 988 GATAACGACTGACAGTCTCTCCGAGTTGCTGCACAGTTG---GACTCTGGGAGTCCAG 1044
OY 362 SerLeuGluHisProGluGluGluAsnGluProSerLeuGlnSerLysLeu---GlnAsp 380
Db 1045 ACTCTTGAAGCCCGGAGAGCTCAGCCGAAGTCTCTGATGATGACCTCCATCTGCC 1104
OY 381 GluAlaAsnTyrHisLeuTyrGly---SerArgMetAspArgGlnThrLysGluGlnPro 399
Db 1105 AGCAGTGGCCAGAGGCTCTCGGGGTGCTCAGTGGACTAGACCTTTCTCCAGAGGA 1164
OY 400 ArgGlnAsnValAlaTyrAsnArgGluGluGluArgArgArgValSerHisAspPro 419
Db 1165 TCGCTGTCATGCTTTTGGAGCGGAAAGCTTC-AACAGGCA-----CCT 1208
OY 420 PheAlaGluGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyr 439
Db 1209 GGGCCCAACAGATCCAGAGAA-----GAAGCAGTGGATGCCATCAT 1253
OY 440 SerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSer-----GlyLeu 455
Db 1254 -----ATCAGGGGACACACAGGAGGTGATGAAGATCCTACAGCCCAAGATGTGACTT 1307

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OY 456 ThrSer----- 457
Db 1308 GGTTCATGACACAGATGCCAGCTGCTGACCTGGCTGTGGAGCGGACAGAGACTG 1367
OY 458 -----GlnProGlnValLeuTyrGlnAsnAsnGlyLeu 468
Db 1368 TGTCAAGTGGCTGCTGTTAACATGATCAACCCCAACCT---GACCAACAGAGAGGCTC 1424
OY 469 Tyr---SerSerHisGlyPheGlyThr----- 476
Db 1425 TACACCTGCAATGATGCTGTGTGAGCGGAGGAGCTGGAATTTGTGAGCTACTGCTAGC 1484
OY 477 -----ArgProLeuAsp--ProGlyThrAlaGlyP 486
Db 1485 CCGAAGACCACTGTCATGCCAAGATGAAACACCAAGTGGCTGCTGCACTTGCCAGC 1544
OY 486 roArgValTrpTyrArgProIleProSerHisMetProSerLeuHisAsnIleProValP 506
Db 1545 CCAGATGGGAGATGAGGCCAGCACAGGCTG-CTGCTAGAG---AAGAACTGCTCTGTCA 1600
OY 506 roGluThrAsnTyrLeuGluLysAsnThrPro 515
Db 1601 ATGAGTGGACTTTGAGGCGGACACACC 1629

RESULT 14
US-09-866-050A-257
; Sequence 257, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions isolated from skin cells
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 3516
; TYPE: DNA
; ORGANISM: Mouse
US-09-866-050A-257

Alignment Scores:
Pred. No.: 1,45e-31 Length: 3516
Score: 410.50 Matches: 164
Percent Similarity: 43.43% Conservative: 84
Best Local Similarity: 28.72% Mismatches: 209
Query Match: 11.58% Indels: 116
DB: 9 Gaps: 25

US-09-981-397A-16 (1-671) x US-09-866-050A-257 (1-3516)
OY 14 SerSerAspPheLeuGluSerAlaGluLeuAspSerGlyGlyPheGlyLysValSerLeu 33
Db 58 CGCGGCGCAATTCGAGAGGCTGGAGAGAGTGGGCTCGGCGGCTTCGGGACGCTACAG 117
OY 34 CysPheHisArgThrGluGluGlyLeuMetIleMetLysThr-----ValTyrLysGly 50
Db 118 GTGCGCCAT-----GTGCACTGGAAGAGTGGCTCGGCAATCAAGTGCCTCG 162
OY 51 ProAsnCys---IleGluHisAsnGlu-----AlaLeuGluGluGluAlaLysMetMet 67
Db 163 CCCAGTCTGCACGCTGCAGACAGGACAGGAAAGATGAGCTCTCTGAGGAGAACTAAGAGATG 222
OY 68 AsnArgLeuArgHisSerArgValValLysLeuLeuGlyValIleIleGluGluGlyLys 87
Db 223 GAGATGGCGCAAGTTCGATACATATCTACCTGTATACGCGAATATCCAGGAA-----CCT 276

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US-09-981-397A-16 (1-671) x US-10-152-661-510 (1-1700)

OY 5 MetSerLeuAsnValIleLysMet-----LysSerSerAspPheLeuGlu 19
 Db 124 CTCTGGATGCTTCTGCAAGTATGCTCAATGGCTGATCATCTCTCTGCGC 183
 OY 20 SerIleGluLeuAspSer-----GlyGlyPheGlyLysValSerLeu 33
 Db 184 TCTGAAAGACTGGAGAACCTAGAGATTGTGGCAAAAGCGGGGTGGAGCCGTGTCGG 243
 OY 34 CysPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGlyProAsnGly 53
 Db 244 GCACGCCACACAGCATGAGACCTTGATGAGACGCAAG----- 282
 OY 54 IleGlnHisAsnGluAlaLeuLeuGlnGluAlaLysMetMetAsnArgLeuArgHisSer 73
 Db 283 ATCGTAAGCTCGAAAGATATCCAGGAGGTGAAGGCTATGCTGAATCTTGTCATGAG 342
 OY 74 ArgValValLysLeuLeuGlyValIleIleGlu---GlnGlyLysTyr----- 88
 Db 343 AACGTCGCTCTCTCTGGGGGTCTACAGAACTCCGAGTGGAGCTACGTGACGGCGG 402
 OY 89 SerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeuLysAlaGluMet 108
 Db 403 GCTCTGTGACAGATGATGAGAAAGCGCTCTCAGGGCTCTGCAACCTTCATGTC 462
 OY 109 SerThrProLeuSerValLysGlyArgIleIleLeuGlnIleIleGlnGlyMetCysTyr 128
 Db 463 CCTCGGGCCCTGCTCTCTCTGCTGCTGCTGCTAGAGAGATGCTGCTGGGATGCTGTC 522
 OY 129 LeuHis-----GlyLysGlyValIleHisLysAspLeuLysProGluAsnIleLeuVal 146
 Db 523 CTACACAGACTGAAACCTTGCTGCTACTGACCGGAGCCTCAAGCCCTCAATGTTCTGCG 582
 OY 147 AspaAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPheLysMetTrpSer 166
 Db 583 GATCCAGAGCTCCAGCCAGATGACAGCTTTGGCTGTCACATTTTCAGGGAGGCTCA 642
 OY 167 LysLeuAsnAsnGlnGluHisAsnGluLeuArgGluValAspGlyThrAlaLysLysAsn 186
 Db 643 CAGTCAGGGTCA-----GGGTCAAGATCGAGACATGCT 675
 OY 187 GlyIleThrLeuTyrTyrMetAlaLeuProGluHisLeuAsnAspValAsnAlaLysProThr 206
 Db 676 GGGGACCCCTGACTTACTTGGCCCCAGAG---CTGTTGATTAATGACGGAAGAGCTTCT 732
 OY 207 GlnLysSerAspValTyrSerPheAlaValLeuThrPalalIlePheHisAsnLysGlu 226
 Db 733 AAAGCAAGTATGTTTACAGTTTGGGCTGCTGCTGACAGTCTGCTGCAAGAGAA 792
 OY 227 Pro-----TyrGluAsnAlaIleCysGlnGlnGlnIle 238
 Db 793 GGTGAGGTGTAGACAGACCTCACAATTCGTGAGAGCAGTGTGAACGGGAG----- 846
 OY 239 MetCysIleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArg 258
 Db 847 -----AGCGACCTCCATTCAGACAGCTCCCGGACAGACCCCTGAG 888
 OY 259 Glu-----IleIleSerLeuMetLysLeuCysTrpGlnAlaAsnProGlu 273
 Db 889 ACTCTGGCTTGAAAGGACTGAAGAGTTAATGACGCATTGCTGAGATTCTGAGCCTTAA 948
 OY 274 AlaArgProThrPheProGlyIleGlnGlnLysPheArgProPheTyrLeuSerGlnLeu 293
 Db 949 GACAGGCCATCTCTCAAGACAGCTGAAATCAAAACCAATATGTTTACATC---CTGCTA 1005
 OY 294 GlnGlnSerValGlnGlnAspValLysSerLeuLys-----LysGluTyrSerAsn 310
 Db 1006 CAGGACAAAGTAGTGTCTGCTCCAGGTAAGCATTAATCTGCTCAGTACAGAAAGC 1065
 OY 311 GlnAsnAlaValValLysArgMetGlnSerLeuGln-----LeuAspCysVal 326

Db 1066 AGTACACAAGATTGTCTGCCAGAGAGTCCAGCCAAAAGGTACAGAGTGCATTGC--- 1122
 OY 327 AlaValProSerSerArgMetAsnSerAlaThrGlnGlnProGlySerLeuHisSerSer 346
 Db 1123 -----CCGAGGGAAACCACTACTTTATGAATGCTGAGCCGCTGCAT----- 1164
 OY 347 GlnGlyLeuGlnMetGlyProValGlnGlnLysThrPheAlaProSerLeuGlnHisPro 366
 Db 1165 -----CTGAGAGAGGCC 1176
 OY 367 GlnGlnGlnAsnGlnProSerSerLeuGlnSerLysLeuGlnAspGlnAlaAsnTyrHisLeu 386
 Db 1177 TCT----- 1179
 OY 387 TyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsn 406
 Db 1180 ---GGATGACTTCTCGAAGAGCTCAAGACTT----- 1209
 OY 407 ArgGlnGlnGlnArgArgArgValSerHisAspProPheAlaGlnGlnArgProTyr 426
 Db 1209 ----- 1209
 OY 427 GlnAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSerSerAlaAlaSerHisGly 446
 Db 1210 -----ACTGAGAGAGAGCA-----AAGAGACATCATTTGCG 1242
 OY 447 AsnAlaValHisGlnProSerGlyLeuThrSerGln-----ProGlnVal 461
 Db 1243 CATGCGACA-----CCAGCAGGAGCATCATCTGACCTTGCGTGGCAGCTCCCAAT 1296
 OY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
 Db 1297 CCACAT-----ACTTTACCTCCAGAGCGCACAAACCTAGGCGCAGCTTACT 1344
 OY 482 GlyThrAlaGlyProArgValTyrPyrArgProIleProSerHisMetProSerLeuHis 501
 Db 1345 GAGACTCCAGGTCTGAC----- 1362
 OY 502 AsnIleProValProGluThrAsn-----TyrLeu 511
 Db 1363 -----CCCCAAAGGATCAGGAGATGAGAAACAGCAATCCTGTCGACAC 1410
 OY 512 GlnAsnThrProThrMetProPheSerSerLeuProProThrAspGlnSerIleLysTyr 531
 Db 1411 TGGAAAGCAGCAAAAT---CCAAATGACAGGCTA-----CAGCTCATT----- 1449
 OY 532 ThrIleTyrAsnSerThrGlyIleGlnIleGlyAlaTyrAsnTyrMetGlnIleGlyGly 551
 Db 1450 GTCTTAACACACTGTCTGAAAGTGCAGATTGCACAACACACTGCATGTCACTA----- 1503
 OY 552 ThrSerSerSerLeuLeuAspSerThrAsnThrAsnPro-----LysGlnGlnProAla 569
 Db 1504 -----CAACCGAAGACTGCTTCCCAAGAGAGGAGCAGCA 1539

Search completed: June 25, 2003, 23:47:51
 Job time : 275 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2003, 16:07:14 ; Search time 43 Seconds

(without alignments)
1500.144 Million cell updates/sec

Title: US-09-981-397a-16

Perfect score: 3545

Sequence: 1 MOPDMSLVNVIKMKSSDFLES.....ALHOCSDRLDLSLIVYSON 671

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR_73:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	3545	100.0	671	2 T09479	serine/threonine p
2	2423.5	68.4	656	2 T09479	receptor interacti
3	346.5	9.8	1367	1 IGHUR1	insulin-like growt
4	343	9.7	467	2 T16579	protein-tyrosine k
5	342.5	9.6	640	2 S23008	insulin-like growt
6	340.5	9.6	855	2 T20082	hypothetical prote
7	338.5	9.5	465	2 T148926	protein-tyrosine k
8	338.5	9.5	505	2 T59296	protein-tyrosine k
9	338	9.5	1371	2 A33837	insulin-like growt
10	337.5	9.5	507	2 A55625	protein-tyrosine k
11	336.5	9.5	848	2 B87950	protein F33E2.2 [1
12	336.5	9.5	1171	2 T12956	hypothetical prote
13	335	9.4	512	1 TYHUIY	protein-tyrosine k
14	335	9.4	829	2 T07406	probable protein k
15	334.5	9.4	1094	2 S49313	protein kinase - s
16	333	9.4	1382	1 INHUR	insulin receptor p
17	332.5	9.4	1372	2 A34157	insulin receptor p
18	331.5	9.4	390	2 T01451	protein kinase hom
19	330.5	9.3	1383	2 A36080	insulin receptor p
20	330.5	9.3	2148	1 A56081	insulin receptor p
21	329	9.3	475	2 T12955	probable protein k
22	329	9.3	1257	2 T00486	serine/threonine-s
23	328.5	9.3	450	1 S15094	protein-tyrosine k
24	328.5	9.3	567	2 JCS957	transforming growt
25	327.5	9.2	1248	2 B96827	hypothetical prote
26	327.5	9.2	2101	2 S57245	insulin receptor (
27	325.5	9.2	507	1 A39339	protein-tyrosine k
28	325	9.2	512	1 A39719	transforming growt
29	325	9.2	606	2 JCS956	transforming growt

30	324.5	9.2	497	1 S43532	protein-tyrosine k
31	323.5	9.1	450	1 JH0559	protein-tyrosine k
32	322	9.1	512	1 I56160	protein-tyrosine k
33	322	9.1	1123	2 A39962	kinase-related tra
34	322	9.1	1125	1 OKURCP	spectact receptor p
35	321.5	9.1	509	1 OKRULK	protein-tyrosine k
36	321.5	9.1	1147	2 F86297	hypothetical prote
37	320.5	9.0	579	2 JCS955	transforming growt
38	319	9.0	650	1 JCI450	fibroblast growth
39	318	9.0	450	2 A41973	protein-tyrosine k
40	318	9.0	942	2 C96574	hypothetical prote
41	317.5	9.0	407	2 G84635	probable protein k
42	317.5	9.0	450	2 T148929	protein-tyrosine k
43	317	8.9	1029	2 H86179	hypothetical prote
44	316.5	8.9	625	1 A43030	protein-tyrosine k
45	316	8.9	829	2 JCS483	fibroblast growth

ALIGNMENTS

RESULT 1									
T09479									
serine/threonine protein kinase (EC 2.7.1.-) RIP - human									
C:Species: Homo sapiens (man)									
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000									
C:Accession: T09479; 138992									
R:Huang, J.; Hsu, H.; Balchwal, V.R.; Goeddel, D.V.									
submitted to the EMBL Data Library, August 1998									
A:Reference number: 216685									
A:Accession: T09479									
A>Status: preliminary; translated from GB/EMBL/DBJ									
A:Molecule type: mRNA									
A:Residues: 1-671 <HUA>									
A:Cross-References: EMBL:U50062; NID:93426026; PID:93426027									
R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.									
Cell 81, 513-523, 1995									
A:Title: RIP: a novel protein containing a death domain that interacts with Fas/Apo-1									
A:Reference number: A56913; MUID:95277838; PMID:7538908									
A:Accession: I38992									
A>Status: preliminary									
A:Molecule type: mRNA									
A:Residues: 300-513, 'S', 515-671 <RES>									
A:Cross-References: EMBL:U25994; NID:9829616; PID:NAC50137.1; PID:9829617									
C:Genetics:									
A:Gene: RIP									
C:Keywords: ATP binding; phosphotransferase									
Query Match									
Best Local Similarity 100.0%; Score 3545; DB 2; length 671;									
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
OY	1	MOPDMSLVNVIKMKSSDFLES	AGGFGKYSLCFHTQGLIMTKVYKGPNCIEHNEAL	60					
DB	1	MOPDMSLVNVIKMKSSDFLES	AGGFGKYSLCFHTQGLIMTKVYKGPNCIEHNEAL	60					
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DB	61	LEEAKMNRRLRSRYKLVGLIIEGKYSLVWEYHEKGNLHVLAENSTPLSVAGRIIL	120						
OY	121	ETIEGMCYILHGKGVYHDKLPENIIVDNDFFHRIKIDGLASPKMMSKLNNEHNLREVD	180						
DB	121	ETIEGMCYILHGKGVYHDKLPENIIVDNDFFHRIKIDGLASPKMMSKLNNEHNLREVD	180						
OY	181	GTAKKNGGLTYMADEHLNDVNAKPTKSDVYSFAVNLMAJFANKEPYENALICEQOLIMC	240						
DB	181	GTAKKNGGLTYMADEHLNDVNAKPTKSDVYSFAVNLMAJFANKEPYENALICEQOLIMC	240						
OY	241	IKSGNRPPVDOTTECCPREITISLMKLCWEANNEAPRTPTGTEKRRPYLSQLESVEED	300						
DB	241	IKSGNRPPVDOTTECCPREITISLMKLCWEANNEAPRTPTGTEKRRPYLSQLESVEED	300						
OY	301	VKSLKKEYSNEAVVAKRMQSLQLDCAVAVSSNSNSATQPGSLHSSQGLGMGPVEESMFA	360						

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Db      301 VKSLRKEYSNENAVYKRMQSLQDCVAVPSSRSNSNATEQPGSLHSSQGLMGPEESWFA 360
QY      361 PSLERHOENEPNLSQSLQDEANHYLYGSRMDROTQOOPRONVAYNREERRRRSHDF 420
Db      361 PSLERHOENEPNLSQSLQDEANHYLYGSRMDROTQOOPRONVAYNREERRRRSHDF 420
QY      421 MOORPYENFONTEGKGYVSSAASHGNVAHQPSGLTSOPQVLYONNGLYSSHGFGTRPLD 480
Db      421 MOORPYENFONTEGKGYVSSAASHGNVAHQPSGLTSOPQVLYONNGLYSSHGFGTRPLD 480
QY      481 PGTAAPRWYRPIPSHMSPLHNPVETNYLGNTPMPFSSLPPTDESIKTYTINSTGIC 540
Db      481 PGTAAPRWYRPIPSHMSPLHNPVETNYLGNTPMPFSSLPPTDESIKTYTINSTGIC 540
QY      541 IGAVYMEIGTSSSLDSTNTNFKKEPAKYOALFDNTTSLTDKHLDPRENLGKHKN 600
Db      541 IGAVYMEIGTSSSLDSTNTNFKKEPAKYOALFDNTTSLTDKHLDPRENLGKHKN 600
QY      601 CARLIGFTQSOIDEIDHDYERDGLKEKYOMLQKVMREGIKGATVGLAQLAHOCSTRD 660
Db      601 CARLIGFTQSOIDEIDHDYERDGLKEKYOMLQKVMREGIKGATVGLAQLAHOCSTRD 660
QY      661 LLSSLIYVSQN 671
Db      661 LLSSLIYVSQN 671

```

RESULT 2

149299

receptor interacting protein RIP - mouse

C:Species: Mus musculus (house mouse)

C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999

C:Accession: 149299

R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.

Cell 81, 513-523, 1995

A:Title: RIP: a novel protein containing a death domain that interacts with Fas/Apo-1 (C

A:Reference number: A56913; MUID:95278783; PMID:7538908

A:Accession: 149299

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-656 <RES>

A:Cross-references: EMBL:U25995; NID:9829618; PIDN:AAB60487.1; PID:9829619

C:Genetics:

A:Gene: RIP

A:Superfamily: protein kinase homology

F.15-293/Domain: protein kinase homology <KIN>

Query Match

Best Local Similarity 68.4%; Score 2423.5; DB 2; Length 656;

Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

```

QY      1 MOPDMSLVIVKMKSSDFLEASLDGSGFGKVSICPHRTQGLIMKTYKGCNCLHNAL 60
Db      1 MOPDMSLVIVKMKSSDFLEASLDGSGFGKVSICPHRTQGLIMKTYKGCNCLHNAL 60
QY      61 LEEAKMNRRLHRSRYVLLGVYIEEGKSYLMEYMEKGNLHVLAKESTPLSYGRTIL 120
Db      61 LEEAKMNRRLHRSRYVLLGVYIEEGKSYLMEYMEKGNLHVLAKESTPLSYGRTIL 120
QY      121 EELGCMCLHDKGVYHKDLKPEMLIVDPFHITKIDLVASAFKTSKLTKEKDKMKQKVS 180
Db      121 EELGCMCLHDKGVYHKDLKPEMLIVDPFHITKIDLVASAFKTSKLTKEKDKMKQKVS 180
QY      181 GTAKK-NGSTLYAPAEHLNDVNAKPTKSDVYSFAVVLMATFANKKEYENALCEQOLIM 239
Db      181 GTAKK-NGSTLYAPAEHLNDVNAKPTKSDVYSFAVVLMATFANKKEYENALCEQOLIM 239
QY      240 CIKSGNRDVEDITCYCPREILISLKLCEANPEARPTPEIEKFRFYLSOLEESVEE 299
Db      240 CIKSGNRDVEDITCYCPREILISLKLCEANPEARPTPEIEKFRFYLSOLEESVEE 299
QY      300 DYKSLKREYSNENAVYKRMQSLQDCVAVPSSRSNSNATEQPGSLHSSQGLMGPEESW 359
Db      300 DYKSLKREYSNENAVYKRMQSLQDCVAVPSSRSNSNATEQPGSLHSSQGLMGPEESW 359

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Db      301 DVASLKEYPDQSPVLQRMFSLQHDQVPLPSPRSNS--EGGSLHSSQGLMGPEESW 358
QY      360 APSLHROENEPNLSQSLQDEANHYLYGSRMDROTQOOPRONVAYNREERRRRSHDP 419
Db      360 APSLHROENEPNLSQSLQDEANHYLYGSRMDROTQOOPRONVAYNREERRRRSHDP 419
QY      420 FAOQRPYENFONTEGKGYVSSAASHGNVAHQPSGLTSOPQVLYONNGLYSSHGFGTRPL 479
Db      420 FAOQRPYENFONTEGKGYVSSAASHGNVAHQPSGLTSOPQVLYONNGLYSSHGFGTRPL 479
QY      480 PGTAAPRWYRPIPSHMSPLHNPVETNYLGNTPMPFSSLPPTDESIKTYTINSTGIC 539
Db      480 PGTAAPRWYRPIPSHMSPLHNPVETNYLGNTPMPFSSLPPTDESIKTYTINSTGIC 539
QY      540 OIGAVYMEIGTSSSLDSTNTNFKKEPAKYOALFDNTTSLTDKHLDPRENLGKHKN 599
Db      540 OIGAVYMEIGTSSSLDSTNTNFKKEPAKYOALFDNTTSLTDKHLDPRENLGKHKN 599
QY      599 OIGAVYMEIGTSSSLDSTNTNFKKEPAKYOALFDNTTSLTDKHLDPRENLGKHKN 644
Db      599 OIGAVYMEIGTSSSLDSTNTNFKKEPAKYOALFDNTTSLTDKHLDPRENLGKHKN 644
QY      600 NCARKLGTQSOIDEIDHDYERDGLKEKYOMLQKVMREGIKGATVGLAQLAHOCSTRD 659
Db      600 NCARKLGTQSOIDEIDHDYERDGLKEKYOMLQKVMREGIKGATVGLAQLAHOCSTRD 659
QY      659 NCARKLGTQSOIDEIDHDYERDGLKEKYOMLQKVMREGIKGATVGLAQLAHOCSTRD 664
Db      659 NCARKLGTQSOIDEIDHDYERDGLKEKYOMLQKVMREGIKGATVGLAQLAHOCSTRD 664
QY      660 DLSSLIYVSQN 671
Db      660 DLSSLIYVSQN 671

```

RESULT 3

149299

Insulin-like growth factor 1 receptor precursor - human

N:Alternate names: IGF-1 receptor

N:Contains: insulin-like growth factor 1 receptor alpha chain; insulin-like growth fa

C:Species: Homo sapiens (man)

C:Date: 24-Jun-1987 #sequence_revision 10-May-1996 #text_change 18-Feb-2000

C:Accession: A25690; B38268; P00159; A54170; B54170

R:Ullrich, A.; Gray, A.; Tam, A.W.; Yang-Feng, T.; Tsudokawa, M.; Collins, C.; Henzel

EMBO J. 5, 2503-2512, 1986

A:Reference number: A25690; MUID:87053815; PMID:2877871

A:Accession: A25690

A:Molecule type: mRNA

A:Residues: 1-1367 <ULL>

A:Cross-references: EMBL:M24599; GB:X04434; NID:933058; PIDN:CAA28030.1; PID:9804990

A:Experimental source: Placenta

A:Note: parts of this sequence were confirmed by peptide sequencing

R:Partanen, J.; Mekelae, T.P.; Alltalo, R.; Lehtvaesalho, H.; Alltalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A:Reference number: A38268; MUID:91062389; PMID:2247464

A:Accession: B38268

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1137-1193 <PAR>

R:Cooke, D.W.; Bankert, L.A.; Roberts Jr., C.T.; LeRoith, D.; Casella, S.J.

Biochem. Biophys. Res. Commun. 177, 1113-1120, 1991

A:Title: Analysis of the human type I insulin-like growth factor receptor promoter re

A:Reference number: P00159; MUID:91282751; PMID:1711844

A:Accession: P00159

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-31 <COO>

A:Cross-references: GB:M69229; NID:9184837; PIDN:AAB5399.1; PID:9184838

R:Kaaya, J.; Paz, I.B.; Maddux, B.A.; Goldfine, I.D.; Hetta, S.A.; Fujita-Yamaguchi,

Biochemistry 32, 13531-13536, 1993

A:Title: Characterization of human placental insulin-like growth factor-I/insulin hpb

A:Reference number: A54170; MUID:94079885; PMID:8257688

A:Accession: A54170

A:Molecule type: protein

A:Experimental source: Placenta

A:Note: sequence extracted from NCBI backbone (NCBIP:141172) and corrected to corres

A:Accession: B54170

A:Molecule type: protein

A:Residues: 741-746, 'X', 748-750 <RA2>
 A:Experimental source: placenta
 C:Genetics:
 A:Gene: GDB:IGFIR
 A:Cross-references: GDB:120082; OMIM:147370
 A:Map position: 15q26.1-15qter
 C:Complex: heterotetramer of 2 alpha and 2 beta chains; alpha and beta chains are derived from the two alpha chains are disulfide bonded; also naturally forms a disulfide bonded hybrid
 C:Function:
 A:Description: membrane glycoprotein that mediates the effects of insulin-like growth hormone (IGF) on the beta chain tyrosine-kinase undergoes autophosphorylation and C:Superfamily: Insulin receptor; protein kinase homology
 C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprotein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-76/Product: insulin-like growth factor 1 receptor alpha chain #status predicted <F>
 F:178-332/Region: cysteine-rich
 F:741-1367/Product: insulin-like growth factor 1 receptor beta chain #status predicted <F>
 F:936-958/Domain: transmembrane #status predicted <TM>
 F:997-1273/Domain: protein kinase homology <KIN>
 F:1005-1013/Region: protein kinase ATP-binding motif
 F:102-135, 244, 314, 417, 438, 534, 607, 622, 640, 756, 764, 900, 913/Binding site: carbohydrate (Asp)
 F:455-488/Disulfide bonds: #status predicted
 F:544/Disulfide bonds: interchain #status predicted
 F:747/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:1033, 1135/Active site: Lys, Asp #status predicted
 F:1161, 1165, 1166, 1346/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)

Query Match 9.8%; Score 346.5; DB 1; Length 1367;
 Best Local Similarity 27.9%; Pred. No. 4,36-09;

Matches 117; Conservative 64; Mismatches 147; Indels 91; Gaps 18;

20 SAELDSGFGKV-----SLCFHRTQGLMIMKTYVKGPNCEIENHALLLEAKMNRRLRS 73
 1002 SRELGGSGFGVYEGVAKGVKDEPTEVRAIKTYNEASMRERIE-FLNEASVKKERENCH 1060
 Db
 74 RYVLLGVIIIEEGKYSLVMEYMEKGNL--MHVLAEMS-----TPLSVKGRIIL--EII 123
 1061 HAVVLLGVVSGOGFTVIMELTRGDLKYLRSIRPEMENNVPVLAPELSKMIQAGEIA 1120
 Oy
 124 EGACVLYHGKGVIRKDLKPELVNDNRHITADIGLASFKMWSKLNNEHNEHLEVDGTA 183
 1121 DGMAYLVANKFVHRDIAARCMVAEDFTVXIGDFGNT-----RDYETDYR 1167
 Db
 184 KKNKGTL--YYMAPEHNDVNAKPTKSDVYSFAVVLMAIFA--NKEPYENALICQQLIMC 240
 1168 KGGKGLPVKRMSESLKD--GVFTTSDVMSFVGLMETATLAEPYQGLSNEQVLRV 1225
 Oy
 241 IKSG--NRPDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKFRPPLYLSOLEESVE 298
 1226 MEGGLDKPD-----NCPMLFELMRMCQYNPKMRPSLEI-----ISSIKEME 1271
 Db
 299 EDVKSLLKKEYSNENAV-----VKRMSQLDCAVAVSSKNSNSATEOPGSLHSSQGL 349
 1272 PGREVSFYYSSEKKLEPEPELDEPENMESVPLD-----PSASSSLPLP--DRHSGH-- 1323
 Oy
 350 GMPVEESWPAFLSHPQENEPS-----LOSKLQDEANV--HUYGSMRDRQTKQRPON 402
 1324 -----KABNGGPGVVLVLRASFDENQPIAHMNGKKNRALLPDPSS 1365
 Db

RESULT 4

156579
 Protein-tyrosine kinase (EC 2.7.1.112) back - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence, revision 26-Jul-1996 #text, change 04-Mar-2000
 C:Accession: 156579
 R:Kuo, S.S.; Moran, P.; Gripp, J.; Armanini, M.; Phillips, H.S.; Goddard, A.; Caras, L.W.
 J. Neurosci. Res. 38, 705-715, 1994
 A:Title: Identification and characterization of Bakt, a predominantly brain-specific not
 A:Reference number: 156579; MUID:95106341; PMID:7807586
 A:Accession: 156579
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA

A:Residues: 1-467 <RES>
 A:Cross-references: GB:L34542; NID:9530157; PIDN:AAA64524.1; PID:9530158
 C:Genetics:
 A:Gene: bakt
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
 C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 F:14-64/Domain: SH2 homology <SH3>
 F:81-170/Domain: SH2 homology <SH2>
 F:192-445/Domain: protein kinase homology <KIN>
 F:200-208/Region: protein kinase ATP-binding motif

Query Match 9.7%; Score 343; DB 2; Length 467;
 Best Local Similarity 33.2%; Pred. No. 1,86-09;

Matches 89; Conservative 47; Mismatches 100; Indels 32; Gaps 9;

21 AELDSGFGKVSCLCFHRTQGLMIMKTYVKGPNCEIENHALLLEAKMNRRLRSVYKL 79
 198 AOIEGEGFAGV-----LQGEYLQKVAVKKIKCDVTAQAFIDETAVMTKLQHRNLVRL 251
 Db
 80 GVIIIEEGKYSLVMEYMEKGNLMHVLKAMSPPLSVKG--RIILEIGMVCYHGKGVYHK 137
 252 GVIIHHGLY-IVMEHVSKNLVNFLRTRGRALYSTQLDPAALVAGMETLESKTLVHR 310
 Oy
 138 DLKPELVNDNRHITADIGLASFKMWSKLNNEHNEHLEVDGTAKKNGTLYMAPEH 197
 311 DLARNILVSDILVAKVSDGLAKAKELRKGLDSSRL-----PVKWPAPEA 355
 Db
 198 LNDVNAKPTKSDVYSFAVVLMAIFA--NKEPYENALICQQLIMCKSGNRPDVTIEYC 256
 356 LK--NGRFSSKSDVMSFVGLLMEVFSYGRAPYK--MSLKESEAVKGYREPPD---SC 409
 Oy
 257 PREIISLMKLCWEANPEARPTFGIEEK 284
 410 PGVHTLMGSCWEAEPSPRPPEKIVK 437
 Db

RESULT 5

523008
 Insulin-like growth factor receptor 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 08-Jun-1994 #sequence, revision 01-Sep-1995 #text, change 18-Jun-1999
 C:Accession: S23008
 R:Sneyers, M.; Kettmann, R.; Messart, S.; Renaville, R.; Burry, A.; Portetel, D.
 DNA Seq. 1, 405-406, 1991
 A:Title: Cloning and characterization of a cDNA encoding the beta-subunit of the bovi
 A:Reference number: S23008; MUID:92119330; PMID:1662995
 A:Accession: S23008
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-640 <SNP>
 A:Cross-references: EMBL:X54980; NID:9433; PIDN:CAA38724.1; PID:9434
 C:Superfamily: Insulin receptor; protein kinase homology
 C:Keywords: ATP; growth factor receptor
 F:270-546/Domain: protein kinase homology <KIN>
 F:278-286/Region: protein kinase ATP-binding motif

Query Match 9.7%; Score 342.5; DB 2; Length 640;
 Best Local Similarity 27.9%; Pred. No. 2,86-09;

Matches 116; Conservative 67; Mismatches 148; Indels 85; Gaps 18;

20 SAELDSGFGKV-----SLCFHRTQGLMIMKTYVKGPNCEIENHALLLEAKMNRRLRS 73
 275 SRELGGSGFGVYEGVAKGVKDEPTEVRAIKTYNEASMRERIE-FLNEASVKKERENCH 333
 Db
 74 RYVLLGVIIIEEGKYSLVMEYMEKGNL--MHVLAEMS-----TPLSVKGRIIL--EII 123
 334 HAVVLLGVVSGOGFTVIMELTRGDLKYLRSIRPEMENNVPVLAPELSKMIQAGEIA 393
 Db
 124 EGACVLYHGKGVIRKDLKPELVNDNRHITADIGLASFKMWSKLNNEHNEHLEVDGTA 183
 394 DGMAYLVANKFVHRDIAARCMVAEDFTVXIGDFGNT-----RDYETDYR 440
 Db
 184 KKNKGTL--YYMAPEHNDVNAKPTKSDVYSFAVVLMAIFA--NKEPYENALICQQLIMC 240
 Oy

Db 441 KGGKILLYRWMSPESLD--GVFTTHSDVMSFGVYLWEIATLADQPYOGLSNEQVLRV 498
 QY 241 IKSG--NRPDVDDITTEYCPREIISLMKLCWEANPEARPTFIEKFRFYISQLEESVE 298
 Db 499 MEGGILLDPD-----NCPDMLPELMRCWOYNPMRPSFLEI-----ISSVKDME 544
 QY 299 EDVKSIRKEYSNNVAVRMOSLDQVAVPSRSNSATTEQPGSLHSSQGLQMGPEESW 358
 Db 545 AGFREVSFYSPEN---KPEPEELD-----EPENNESV-----PLDPSA 582
 QY 359 FAPSLIEHP-----QEENEPS-----LOSKLQDEANY-HLYGSRMDROTKOOPRON 402
 Db 583 SSASLPLDRHSGHKAENGPGGVLYLRASPEDERQYAHMNGRKRENERALPLPOSS 638

RESULT 6

T20082

hypothetical protein F33E2.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T20082; T21703

R:Lennard, N.

submitted to the EMBL Data Library, April 1998

A:Reference number: Z19221

A:Accession: T20082

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-855 <WLI>

A:CROSS-references: EMBL:AL022593; PIDN:CA18635.2; GSPDB:GN00019; CESP:F33E2.2

A:Experimental source: clone C4959

A:Reference number: Z19461

A:Accession: T21703

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-855 <WLI>

A:CROSS-references: EMBL:284574; PIDN:CA06544.2; GSPDB:GN00019; CESP:F33E2.2

A:Experimental source: clone F33E2

C:Genetics:

A:Gene: CESP:F33E2.2

A:Map position: 1

A:Introns: 47/2; 213/2; 263/2; 366/3; 494/1; 547/3; 608/1; 826/3

Query Match 9.6%; Score 340.5; DB 2; Length 855;
 Best Local Similarity 22.9%; Pred. No. 4.8e-09;
 Matches 162; Conservative 94; Mismatches 259; Indels 191; Gaps 28;

QY 13 KSSD-----FLESALDSGGFGVYSLCFHRTQGLMTKTVYKGPNCIEHNEALLE-EAK 65
 Db 49 KSEDELWEIPDAISELEMLGSGGAVF---RQLENRVY-----AVKKVNOQKEPEIK 100
 QY 66 MNNRLRSRRVYKLLGVIIEEGKYSILVMEYMEKGNIMHYLKAEMSTPLSVKRILILEEG 125
 Db 101 HLRHLRHONITEFGVSCSPCYIVMEYCSKQGLCTVLCRNRTITRELFAPQWKEADG 160
 QY 126 MCVLHGKGVTHDKLPENITLVNDPFHIKTIADIGLASFEMWSKLNNHEEHNEAREVDGTAKK 185
 Db 161 MHYHLHOKVTHIRDLKSPNILLSADSTIKICDFGTSHQ-----KRDSTIMS 207
 QY 186 NGGLTYMAPRHLNDVNAPK-TEKSDVYSFAVNLMAIFANKEPEYNAICEQOLIMCISG 244
 Db 208 FCGVTSVMAPEM--IKKPCNEKRVYVSFGVVLMEMLTRETPEYAN-IAQVAIIFGVGTN 263
 QY 245 --NRPDVDDITTEYCPREIISLMKLCWEANPEARPTFIEKFRFYISQLEESVE 295
 Db 264 ILSLP-----MPEAPKGLVILIKQCLSQKGRNRSFSHIROHWEIPELPEFEMEEMOL 319
 QY 296 -----SVEEDVKSIRKEYSNNVAVRMOSLDQVAVPSRSNSATTEQPGSLHSSQGLQMGPEESW 358
 Db 320 AMSYREFAKCIQYPTVTRDGHGPKSAFAMEEELQKRRHEOLNHIIDIRIMYEMKL--- 376

QY 327 AVPSRSNSATTEQPGSLHSSQGLQMGPEESWFAPSLEHPQEEENPSLOSKLQDEANYHL 386
 Db 377 ---KRTKMKDKLOGCTTELKKESELA-EWEDLTEREOMHONNSKAAVAPRAQIRG 431
 QY 387 YGSR---MDROTQOPRONVAYN-REEERRRRVSHDPAQORPEYENFQNTGKGYVSS 441
 Db 432 YPNEGIDMSDEDEQPCRGSPYRCSTNTSSSGVSSPFSHQ---SSRSRSGOQTRSE 488
 QY 442 AA-----SHGNAVHPSSLTS----- 457
 Db 489 GANPKILRNDALIRHSGSYWETLGARGSPARDGFSODSGMSAGASCTAINGGQOV 548
 QY 458 -QPGVLYON-NGIYSSHEFGTR-----PLDGTGTA--GPVWY-PIPSHPSLHNI---P 504
 Db 549 CYSOTLYRNGDGRNSDGRFASRRRVSYVKNSTAVPGQPVFTTDSRRV--HGVISCS 606
 QY 505 VPETNYLGNPTMPRSSLP-----PTDESITYTNSGTGIGTIGAYNMEIG 550
 Db 607 SPRSSSKLRNSYSPSRNAPHOLEGCCAHARAPRAKSIAVPM----- 649
 QY 551 GTSSSLDSTMTNKEEPAAYQALFDNTTSLTQKHLDPTENLCK 596
 Db 650 -TSS-----RASPPTYDNDFENAESFVDESPKRLNLEK 685

RESULT 7

I48926

protein-tyrosine kinase (EC 2.7.1.112) CLK - mouse

N:Alternate names: csk-type protein-tyrosine kinase

C:Species: Mus musculus (house mouse)

C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 04-Feb-2000

C:Accession: I48926

R:Klagges, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.; Penhallow, R.C.

Proc. Natl. Acad. Sci. U.S.A. 91, 2597-2601, 1994

A:Title: CLK: a protein-tyrosine kinase related to Csk that defines an enzyme family.

A:Reference number: A53469; MUID:94195789; PMID:7511815

A:Accession: I48926

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-465 <RES>

A:CROSS-references: EMBL:U05210; NID:9450232; PIDN:AA18829.1; PID:9450233

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH

C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F:13-63/Domain: SH3 homology <SH3>

F:80-169/Domain: SH2 homology <SH2>

F:191-443/Domain: protein kinase homology <KIN>

F:195-207/Region: protein kinase ATP-binding motif

Query Match 9.5%; Score 338.5; DB 2; Length 465;
 Best Local Similarity 33.6%; Pred. No. 3e-09;
 Matches 90; Conservative 46; Mismatches 99; Indels 33; Gaps 10;

QY 21 AELDSGGFGVYSLCFHRTQGLMT-MKTVYKGPNCIEHNEALLEEAKMMNRLRSRVKLL 79
 Db 197 AQIEGEFGAV-----LQGEYLGQKAVANNIKCDVTAQAFLEDETAVMTLQHRNEVRL 250
 QY 80 GVIIIEGKYSILVMEYMEKGNIMHYLKAEMSTPLSVK--RLIIIEIGMGVLYGKGYIHK 137
 Db 251 GVILHGLY-IVMHVYSKGNLVNLFRTGRALVYSTQLOLPAHLVAGMEYLSKKLIVHR 309
 QY 138 LKRPENILVNDPFHIKTIADIGLASFEMWSKLNNHEEHNEAREVDGTAKKNGTLYYNAPEH 197
 Db 310 DLARNILIVSHDLVAKVSDGLK-----AERGGDSSRL---PVKWTAPRA 353
 QY 198 LNDVNAPTEKSDVYSFAVNLMAIFA-NKEPEYNAICEQOLIMCISGNRPDVTTEYC 256
 Db 354 LK--NGRESSKSDVMSFGVVLMEYFSYGRAPYK-MSLKEVSAVEAGKYMPEPD--GC 407
 QY 257 PREIISLMKLCWEANPEARPTFIEK 284
 Db 408 PGVHTILMGSCWEAEPARRPFRKIVK 435

RESULT 8
159296

protein-tyrosine kinase (EC 2.7.1.112), megakaryocyte-associated - mouse

N:Alternate names: ctk

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence, revision 02-Jul-1996 #text, change 04-Feb-2000

C:Accession: 159296; 158407; B55625; 149621

R:Chow, L.M.L.; Jarvis, C.D.; Hu, Q.; Nye, S.H.; Gervais, F.G.; Veillette, A.; Mattis, L. Proc. Natl. Acad. Sci. U.S.A. 91, 4975-4979, 1994

A:Title: Ntk: A csk-related protein-tyrosine kinase expressed in brain and T lymphocytes

A:Reference number: 159296; MUID:94255451; PMID:8197166

A:Accession: 159296

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-505 <RES>

A:Cross-references: GB:I27738; NID:9507289; PIDN:AAB59677.1; PID:9507290

R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C. Oncogene 9, 3437-3448, 1994

A:Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine protein

A:Reference number: 158407; MUID:95060800; PMID:7970703

A:Accession: 158407

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-43 <REZ>

A:Cross-references: GB:I33339; NID:9609536; PIDN:AAA64431.1; PID:9609537

R:Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avraham, J. Biol. Chem. 270, 1833-1842, 1995

A:Title: Structural and functional studies of the intracellular tyrosine kinase MATK gen

A:Reference number: A55625; MUID:95130565; PMID:7530249

A:Accession: B55625

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 41-505 <AVR>

R:Kaneko, Y.; Monoguchi, K.; Fukuyama, H.; Takano, S.; Hirasnitsuji, H.; Nishiyama, H.; Oncogene 10, 945-952, 1995

A:Title: Presence of alternative 5' untranslated sequences and identification of cells e

A:Reference number: 149621; MUID:95206787; PMID:7898936

A:Accession: 149621

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 41-505 <RE3>

A:Cross-references: GB:D45243; NID:9639858; PIDN:BA081199.1; PID:9639859

C:Genetics:

A:Insertions: 23/3

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

Db 448 PGSVHTLMGSCWAEAPARRPFRKIVER 475

RESULT 9
A33837

N:Contains: insulin-like growth factor I receptor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Mar-1990 #sequence, revision 03-Nov-1995 #text, change 21-Jul-2000

A:Accession: JC2461; A33837; PC1131

R:Pedrini, M.T.; Giordano, F.; Smith, R.J. Biochem. Biophys. Res. Commun. 202, 1038-1046, 1994

A:Title: cDNA cloning of the rat IGF I receptor: Structural analysis of rat and human

A:Reference number: JC2461; MUID:94324926; PMID:8048916

A:Accession: JC2461

A:Molecule type: mRNA

A:Residues: 1-1371 <PED>

R:Werner, H.; Molochuk, M.; Adamo, M.; Shen-Or, Z.; Roberts Jr., C.T.; LeRoith, D. Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989

A:Title: Developmental regulation of the rat insulin-like growth factor I receptor ge

A:Reference number: A33837; MUID:90017496; PMID:2477843

A:Accession: A33837

A:Molecule type: mRNA

A:Residues: 1-364 <MER>

A:Cross-references: GB:M27293

R:Knuchal, H.; Jodo, K.; Ohta, M.; Kawasaki, T.; Itoh, N. Biochem. Biophys. Res. Commun. 187, 934-939, 1992

A:Title: A new member of the insulin receptor family, insulin receptor-related recept

A:Reference number: PC1130; MUID:92412145; PMID:1530648

A:Accession: PC1131

A:Molecule type: mRNA

A:Residues: 913-964, 'PY', 987-1017 <KUN>

A:Cross-references: GB:D12679; NID:9220918; PIDN:BA020983.1; PID:94433359

C:Superfamily: insulin receptor; protein kinase homology

C:Keywords: Arp; growth factor receptor; kinase-related transforming protein; transme

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-741/Product: insulin-like growth factor I alpha chain #status predicted <IG>

F:742-1371/Product: insulin-like growth factor I beta chain #status predicted <IGB>

F:937-959/Domain: transmembrane #status predicted <TM>

F:971-974/Region: GPXY motif

F:978-981/Region: NPXY motif

F:998-1275/Domain: protein kinase homology <KIN>

F:1006-1014/Region: protein kinase ATP-binding motif

Query Match 9.5%, Score 338; DB 2; Length 1371;
Best local similarity 27.2%, Pred. No. 1.1e-08;
Matches 115; Conservative 65; Mismatches 143; Indels 100; Gaps 19;

22 ELDSGGFGKY-----SICFHRTQGLMIMKTYKGPNCIEHNEALLEBAKMMNRLRHRSRV 75

Db 1005 ELGGSGFEGVYEGVAKGVKDEPTEVAIKTVNAASMKREIE-FLNDAVSKFENGHV 1063

QY 76 VKLGVILIEEGKYSLVMEYMEKGNLMHVKLA-----EMSTPLSVKGRITL 120

Db 1064 VRLGVVSQGPVLIVMLMTRGLDKSLRSLREVEQNNTVLIPPSLKTIQAG----- 1119

QY 121 ELIEGMCYLHKGVIHDKLPENILVNDPFIKTIADGLASFVKMSKLNNEHNEHLEVD 180

Db 1120 ELADGMAYLANKKFEVHRDLAARNCVAAEDFVTKIGDFQMT-----RDIVETD 1166

QY 181 GTAKKNGTLL--YMAPRHLMDVNAKPEKSDVSPAVVLAIFA-NKEPYENALICEQL 237

Db 1167 YRRGGKGLPLVRWMSPESLD--GVFTSHDSVSGFVLAWEIATLAEQPYQGLSNEOVL 1224

QY 238 IMCKISG--NRPOVDITREYCPREILISLKCWENAPARPTF-----PGIEKFRP----- 287

Db 1225 RFVWEGGLDKPD-----NCPDALFELMRKQWYNPRMRSFLEIIGSIDMEHPSPQ 1278

QY 288 --FTLSQLESVEEDVSLKREYSENAVAVRMOSLOLDCVAVPSRSNSATEOPGSLHS 345

Db 1279 VSFYSEENKPPPEDEIEMTELEPEN-----MSVPLD-----PSASSASL----- 1320

OY 346 SOGLGMPVEESWEPADLEHP--QEENEPS---LQSKLQDEANY-HLVGSRMDROTKOOP 399
 Db 1321 -----PLPE-----RHSGHKAENGCVLVLTRASPDROPYAMNNGRANERLPLP 1366
 OY 400 RON 402
 Db 1367 QSS 1369

RESULT 10

A55625
 protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
 M:Alternate names: hematopoietic consensus tyrosine-lacking (HYL) non-receptor tyrosine
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 26-May-2000
 C:Accession: A55625; S45333; 158397; T46323
 R:Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avraham, J. Biol. Chem. 270, 1833-1842, 1995
 A:Title: Structural and functional studies of the intracellular tyrosine kinase MATK ger
 A:Reference number: A55625; MUID:95130565; PMID:7530249
 A:Accession: A55625
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-507 <AVR>
 A:Cross-references: GB:S75164; NID:9896217; PIDN:AC60645.1; PID:9896220
 R:Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.; Suda, T.
 Oncogene 9, 1155-1161, 1994
 A:Title: Molecular cloning of a novel non-receptor tyrosine kinase, HYL (hematopoietic C
 A:Reference number: S45333; MUID:94181267; PMID:8134117
 A:Accession: S45333
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-507 <SAC>
 A:Cross-references: EMBL:X77278; NID:9471312; PIDN:CA54493.1; PID:9557272
 R:McVicar, D.W.; Lal, B.R.; Lloyd, A.; Kawamura, M.; Chen, Y.Q.; Zhang, X.; Staples, J.E
 Oncogene 9, 2037-2044, 1994
 A:Title: Molecular cloning of 1sk, a carboxyl-terminal src kinase (csk) related gene, ex
 A:Reference number: 158397; MUID:94268844; PMID:7516063
 A:Accession: 158397
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 42-149, 'GG', 152-160, 'T', 162-288, 'C', 261-296, 'D', 298-336, 'R', 338-362, 'E', 364-
 R:Duesterhoft, A.; Lauber, J.; Mewes, H.W.; Well, B.; Wiemann, S.
 Submitted to the Protein Sequence Database, January 2000
 A:Reference number: 223036
 A:Accession: T46323
 A:Molecule type: mRNA
 A:Residues: 'GNGATPASKCSRDRLGVCRLAEALLGAGAGSGCAPPCQ', 25-507 <AAA>
 A:Cross-references: EMBL:AL137754
 A:Experimental source: adult testis; clone DKFZp434N1212
 C:Comment: For an alternative splice form, see PIR:A49865.
 C:Genetics:
 A:Gene: GDB:MATK; 1sk
 A:Cross-references: GDB:304667
 A:Map position: 19p13.3-19p13.3
 A>Note: DKFZp434N1212.1
 C:Superfamily: protein-tyrosine kinase src; protein-tyrosine homology: SH2 homology: SH3 h
 F:55-105/Domain: SH3 homology <SH3>
 F:123-211/Domain: SH2 homology <SH2>
 F:233-485/Domain: protein kinase homology <KIN>
 F:241-249/Region: protein kinase ATP-binding motif

Query Match 9.5%; Score 337.5; DB 2; Length 507;
 Best Local Similarity 32.6%; Pred. No. 3.7e-09;
 Matches 90; Conservative 47; Mismatches 90; Indels 49; Gaps 11;

OY 21 AELDSGGFGKYSICFHTROGLMI-MKTVYKGPNCIEHNEALLLEAKMMRLRHRSRYVLL 79
 Db 239 AQLGEGGAV-----LQGEYLGQKVAVNKIKCDVNAQAFDLDTAVMTKQHENVRL 292

OY 80 GVILIEGKSYLMEYMEKGNLMHVLAKEMSTPLSVKGRIT-----LETIEGMYL 129
 Db 293 GVILHGLX-IMYEHVSKNLVNFLE-----TRGALVNTAQLLOFSLHVAAGMYL 343
 OY 130 HGKVIHNDLPENILVNDPFHKLADGLASFMMKSKLNNEHNELEVDGTAKNGT 189
 Db 344 ESKKLVHRDLAARNILVSEDLVAKYSDFGLAK-----AERGLDSSRL-----P 387
 OY 190 LYMAPEHNDVNAKPTESDYVSFAVYLMALFA-NKEPYENATEOOLIMCIGKSNPD 248
 Db 388 VKMTAPEALK--HGFTSKSDVMSFGLLMEVFSYGRAPYK-MSLKEVSEAVEKGYRME 444
 OY 249 VDDITEYCPREITISLMKLCWEANPEARPPFGIEEK 284
 Db 445 P---PECGGPHVILMSSQWEAEPRARRPRFKLAEK 477

RESULT 11

B87950
 protein F33E2.2 (imported) - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: B87950
 R:anonymus, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A>Note: see webbed genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C-
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
 A:Accession: B87950
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-848 <STO>
 A:Cross-references: GB:chr_I; PIDN:CAB06544.1; PID:93876653; GSPDB:GN00019; CESP:F33E
 C:Genetics:
 A:Gene: F33E2.2
 A:Map position: 1

Query Match 9.5%; Score 336.5; DB 2; Length 848;
 Best Local Similarity 24.8%; Pred. No. 7.4e-09;
 Matches 127; Conservative 75; Mismatches 206; Indels 105; Gaps 18;

OY 13 KSSD-----FLESALDSGGFGKYSICFHTROGLMIKTVYKGPNCIEHNEALL-EAK 65
 Db 49 KSEDELWEIPPDALSELMLGSGGAYF---RQLENRVY-----AVKKNOJLKEFLIK 100
 OY 66 MMRNRHRSRYVLLGVITIEEYKYSILWEYMEKGNLMHVLAKEMSTPLSVKGRITLIEEG 125
 Db 101 HLRLRHONILIEFLGVCSPCYIVMEYCSKGLCTVLCASRNTITRELFQAWKETADG 160
 OY 126 MCVLHGKGVIRKDKPENIILVNDPFHKLADGLASFMMKSKLNNEHNELEVDGTAKK 185
 Db 161 MHYLLHOKVIRHDLKSPNIIISAEOSTIKICDFGSHMO-----KKMDSTWMS 207
 OY 186 NGTLYYMAPHLNDVNAKP--TEKSDVYSFAVYLMATFANKPEYENALICEOOLIMCJRSK 244
 Db 208 FCGTVSWMAPEM---IKKQPCNEKVDVYSFEGVILMEMLTRETPTAYN-IAOMAILIEGCTN 263
 OY 245 --NRPDVDDITEYCPREITISLMKLCWEANPEARPPFGIE---EKRPFLYSOLEE--- 295
 Db 264 ILSLP---MPEAPKGLVILIKOCLSQKGRNRPFSHIRQHWIRFPELFEEMEQUL 319
 OY 296 -----SVEEDYKSLKREYSENMNVVRMOSLOLDCV 326
 Db 320 AMDSYREFACIQPTVTYTRDHGGPKSAFAWEDEIQKRHHQDLNHIIDINNMEMKL--- 376
 OY 327 AVPSRSNSATQDPGSLHSSQGLCMGPVEESWEPASLEHPQEENEPSLQSKLQDEANYHL 386
 Db 377 ---KRTNKMKDKLQGGFTTELKLESELAE-WEEDLTEROMHNOQNSPKAVAPRAOLRG 431
 OY 387 YGSR---MDROTQOPRONAVYN-REERRRRYSHPFAOQRPYENFQNTTECKGTAYSS 441
 Db 432 YPNEGIDYDMSDEVDYQPCRGSPYRCNSTSSSGVOSSPFROS-----SS 476

R:Wang, Y.

submitted to the EMBL Data Library, May 1997

A:Reference number: Z16016

A:Accession: T07406

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-829 <MAN>

A:Cross-references: EMBL:Y13273; NID:e1050452; PIDN:CAA73722.1; PID:e34294

A:Experimental source: strain UC82B; sub-species Mill

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 9.4%; Score 335; DB 2; Length 829;
 Best Local Similarity 29.7%; Pred. No. 8.5e-09;
 Matches 92; Conservative 63; Mismatches 123; Indels 32; Gaps 11;

QY 4 DMSLVNIMKSSDFLESAGELDSGFGKVSICFHRTQ---GLIMKTYKKGNCNEHNDAL 60
 Db 542 DLVEEFNIPWINDILMEKIGAGSFGTV---HRGDMHGSVAVAKILMEODFAERLKEF 597
 QY 61 LEEAKMNNRLRHSNVVLLGVIIIEGKYSLVMEYMEKGNLMHVL-KAEMSTPLSVKGRRI 119
 Db 598 LREVALMKRLRHPIVLEMGAVIOPNLSITETVLSGSLYRLHLKRGAREVLDERRRLC 657
 QY 120 L-EETEGMCYLHGKG--VIHKDLKPNIIIVDNDPHIKINDGLASKFMMSKLNNEHNE 175
 Db 658 MAYDVANGMNYLHKRNPPIVHRDLKSPNLLVDKKYIVKIDFGLSRKANTFL----- 710
 QY 176 LREVDGTAKKNGSTLYYMAPEHNDVNAKPT-EKSDVYSFAVVLMAIFANKPEYNAICE 234
 Db 711 -----SSKYAACTPEMAPEVIRD--EPSNKSQVDSYGVILMELATTLQOQW-NKLN 760
 QY 235 QOLIMCIKSGNRDPVDITFCPREIISLMKLCWEANPEARPTFGIEEKFREPLYSOLE 294
 Db 761 POYIAAV-GFNRRRLDIPSDLP-QVAIIIEACMANEPMKRPFSFTIMDLRPHLKSPLP 818
 QY 295 ESYEDVDKSL 304
 Db 819 PEGHTDMQLL 828

RESULT 15

S49313

protein kinase - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum

C>Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 24-Sep-1999

C:Accession: S52076; S49313

R:Wetterauer, B.W.; Hamker, U.; von Haeseler, A.; MacWilliams, H.K.; Simon, M.N.; Veron, A.; Title: A protein kinase from Dictyostelium discoideum with an unusual acidic repeat do

A:Reference number: S52076; MUID:95161460; PMID:7857991

A:Accession: S52076

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1094 <WE2>

A:Cross-references: EMBL:Z37981; NID:9551445; PIDN:CAA86053.1; PID:9551446

C:Genetics:

A:Introns: 35/3; 104/1; 166/2

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C:Keywords: ATP

F:20-281/Domain: protein kinase homology <KIN>

F:28-36/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 9.4%; Score 334.5; DB 2; Length 1094;

Matches 123; Conservative 84; Mismatches 167; Indels 173; Gaps 20;

QY 10 IKMSSDFLESAGELDSGFGKVSICFHRTQGLIMKTYKKG-----PNCIE 55
 Db 17 IKYEDDFI--SELGSGGFGKV-----FKGEYLCAVPAVAKIKIHILLDDPNRVD 62
 QY 56 HNEALLLEAKMNNRLRHSNVVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAE-MSTPLSV 114
 Db 63 LEKFLNREIETIKLFTHPNVIQFVIGISENNCILEFIVTELLIEGGDLYLKNQSIDLPWFL 122

QY 115 KGRITLLETIGMCYLHGKGVIIHKDLKPNIIIVDNDPHIKINDGLASKFMMSKLNNEHNE 174
 Db 123 RANIALDVSLAMSYLHRSKSIYHRDLKSTNLLVDKMKIKVDFGFA-----RIYEDNN 176
 QY 175 ELREVDGTAKKNGSTLYYMAPEHNDVNAKPTKESDVYSFAVVLMAIFANKPE----- 227
 Db 177 KSMITCGTDN-----WMSPEMTGLDY--DEKSDIFSFGIVLEIILISRVKPAAPYMRDA 227
 QY 228 ---YENALCEQOLIMCIKSGNRDPVDITFCPREIISLMKLCWEANPEARPTFGIEEK 284
 Db 228 SFGLAEDIVRNQL-----IPTCPESLIDLTFTNCCSVDPNNRPSFEKISQT 273
 QY 285 FRPFTLSQLESVEED-----KRMQSLQDLCVAVPSSRSNATPEQSLHSSQGLGMPVEES 357
 Db 274 ---LKOIKTTLDSNIVYPEIRDFEQOKISTTNGNKKQNGAPKINNLPLOYSNNNN 328
 QY 315 V-----KRMQSLQDLCVAVPSSRSNATPEQSLHSSQGLGMPVEES 357
 Db 329 IYDDDDDDDDDDNDSEFPREYS-----DNSNSVVTLESNSNSNSTINGEQEQEQ 380
 QY 358 WFAPSLEHPQENEPSSQSLQDDEANYHLYGS-----RMDROTQO--PRON 402
 Db 381 EQOQOQOQVKEERDEGEIE--QDDNIEVYDSIQKLEHOKELLERONQOEGSTDEN 437
 QY 403 VAYNKEER-----RRRYS--HDPFAQORPY-----ENFQTEGKQTVY 439
 Db 438 EYVEQEEEBEEDDEEQVISTPAKKRISFGODTFHVEAVRTDDEDDDEDEEBEGDEX 497
 QY 440 SSAASHG 446
 Db 498 ----DHG 500

Search completed: June 21, 2003, 16:15:38
 Job time: 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2003, 15:51:05 ; Search time 26 Seconds
(Without alignments)
1070.408 Million cell updates/sec

Title: US-09-981-397A-16

Perfect score: 3545
Sequence: 1 MOPDMSLNVIKMKSSDFLES.....ALHQCSDLLSLIYVSON 671

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3545	100.0	671	1 RIK1_HUMAN	Q13546 homo sapien
2	2423.5	68.4	656	1 RIK1_MOUSE	O60855 mus musculu
3	423	11.9	518	1 RIK3_HUMAN	O95712 homo sapien
4	404.5	11.4	478	1 RIK3_RAT	O92265 rattus norv
5	401.5	11.3	486	1 RIK3_MOUSE	O99210 mus musculu
6	374	10.6	539	1 RIK2_MOUSE	P58801 mus musculu
7	371	10.5	540	1 RIK2_HUMAN	O43353 h receptor-
8	370.5	10.5	832	1 ANR3_HUMAN	P57078 homo sapien
9	346.5	9.8	1367	1 IGIR_HUMAN	P08069 homo sapien
10	343	9.7	467	1 MATK_RAT	P41243 rattus norv
11	342.5	9.7	640	1 IGIR_BOVIN	O05688 bos taurus
12	339.5	9.6	1370	1 IGIR_RAT	P24062 rattus norv
13	338.5	9.5	505	1 MATK_MOUSE	P41242 mus musculu
14	338	9.5	1373	1 IGIR_MOUSE	O60751 mus musculu
15	337.5	9.5	507	1 MATK_HUMAN	P42679 homo sapien
16	335	9.4	511	1 LYN_HUMAN	P07948 homo sapien
17	333	9.4	1382	1 INSR_HUMAN	P06213 homo sapien
18	332.5	9.4	1372	1 INSR_MOUSE	P15208 mus musculu
19	330.5	9.3	1383	1 INSR_RAT	P15127 rattus norv
20	330	9.3	511	1 LYN_MOUSE	P25911 mus musculu
21	328.5	9.3	450	1 CSK_RAT	P32577 rattus norv
22	327.5	9.2	2146	1 INSR_DROME	P09208 drosophila
23	325.5	9.2	507	1 LCK_CHICK	P42663 gallus gall
24	325	9.2	606	1 M3K7_HUMAN	O43318 homo sapien
25	324.5	9.2	497	1 SPK1_DGCT	P42667 dugesia tlg
26	323.5	9.1	450	1 CSK_HUMAN	P41240 homo sapien
27	322.5	9.1	579	1 M3K7_MOUSE	O62073 mus musculu
28	322	9.1	511	1 LYN_RAT	O07014 rattus norv
29	322	9.1	1123	1 ABL1_MOUSE	P00520 mus musculu
30	322	9.1	1125	1 CYG5_STRPU	P16065 Strongyloce
31	321.5	9.1	508	1 LCK_HUMAN	P06239 homo sapien
32	318	9.0	450	1 CSK_CHICK	P41239 gallus gall
33	317.5	9.0	450	1 CSK_MOUSE	P41241 mus musculu

34	316.5	8.9	504	1 HCK_MACFA	O95m30 macaca fasc
35	316.5	8.9	625	1 ITR_MOUSE	O03526 mus musculu
36	315.5	8.9	503	1 HCK_RAT	P50545 rattus norv
37	315	8.9	393	1 M3K7_DROME	P83104 drosophila
38	315	8.9	1182	1 ABL2_HUMAN	P42664 homo sapien
39	313.5	8.8	1607	1 MIPR_LYMT	O25410 lymnaea sta
40	313	8.8	1300	1 IRR_MOUSE	O9w14 mus musculu
41	312.5	8.8	524	1 HCK_MOUSE	P08103 mus musculu
42	311.5	8.8	526	1 HCK_HUMAN	P08631 homo sapien
43	311	8.8	812	1 FGRL_XENLA	P22182 xenopus lae
44	311	8.8	986	1 CYGR_ARBP	P11528 arbdacia pun
45	310.5	8.8	1297	1 IRR_HUMAN	P14616 homo sapien

ALIGNMENTS

RESULT 1
RIK1_HUMAN STANDARD; PRT; 671 AA.
ID RIK1_HUMAN
AC Q13546: Q13180:
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.-)
DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)
DE (Receptor interacting protein).
GN RIKP1 OR RIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=umbilical vein endothelial cells;
RX MEDLINE=96200892; PubMed=6612133;
RA Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;
RT "TNF-dependent recruitment of the protein kinase RIP to the TNF
receptor-1 signaling complex.";
RL Immunity 4:367-396(1996).
RN [2]
RP REVISION TO 120.
RA Huang J., Hsu H., Baichwal V.R., Goeddel D.V.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE OF 300-671 FROM N.A.
RX MEDLINE=95277838; PubMed=7538908;
RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
RT "RIP: a novel protein containing a death domain that interacts with
Fas/ADO-1 (CD95) in yeast and causes cell death.";
RL Cell 81:513-523(1995).
CC -!- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND
INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFR1 IN A TNF-
DEPENDENT PROCESS. REQUIRED FOR TNFR1 ACTIVATION OF NF-KAPPA B.
CC -!- SIMILARITY: BELONGS TO THE SRR/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U50062; AAC32232.1; -
DR EMBL: U25994; AAC50137.1; -
DR HSSP: P08631; IAD5.
DR Genew: HGNC:10019; RIKP1.
DR MIM: 603453; -
DR InterPro: IPR000488; Death.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR004040; Srv_pkinase.

DR InterPro: IPR002290; Ser thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00531; death; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00221; STYKC; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding; Apoptosis.
 KW Apoptosis.
 FT DOMAIN 17 289
 FT NP_BIND 23 31
 FT BINDING 49 49
 FT ACT_SITE 138 138
 FT DOMAIN 583 669
 FT DOMAIN 411 414
 FT CONFLICT 514 514
 FT SEQUENCE 671 AA: 75958 MW: 75958 MW: BAD04E7E70456ABE CRC64;

Query Match 100.0%; Score 3545; DB 1; Length 671;
 Best Local Similarity 100.0%; Pred. No. 1.7e-201;
 Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOPDMSLVINIKKSSDFLESALDSGGFGKVSICFHRTOGLIMIKTVYKGPNCIEHNEAL 60
 DB 1 MOPDMSLVINIKKSSDFLESALDSGGFGKVSICFHRTOGLIMIKTVYKGPNCIEHNEAL 60
 QY 61 LEEAKMMNRLRHSRVKLLGVIIIEGKYSLVMEYMEKGLMVLAKEMSTPLSVGRILL 120
 DB 61 LEEAKMMNRLRHSRVKLLGVIIIEGKYSLVMEYMEKGLMVLAKEMSTPLSVGRILL 120
 QY 121 EIIIEGMYLHGKGVIIHKDLKPEINILVNDFFHIKIDLGLASFKMSKLNNEENELREVD 180
 DB 121 EIIIEGMYLHGKGVIIHKDLKPEINILVNDFFHIKIDLGLASFKMSKLNNEENELREVD 180
 QY 121 EIIIEGMYLHGKGVIIHKDLKPEINILVNDFFHIKIDLGLASFKMSKLNNEENELREVD 180
 DB 121 EIIIEGMYLHGKGVIIHKDLKPEINILVNDFFHIKIDLGLASFKMSKLNNEENELREVD 180
 QY 181 GTAKNGGCTIYMAEHLNDVAKRTEKSDVSPFVYVIMAFRANKPEYENALICEQOLIMC 240
 DB 181 GTAKNGGCTIYMAEHLNDVAKRTEKSDVSPFVYVIMAFRANKPEYENALICEQOLIMC 240
 QY 181 GTAKNGGCTIYMAEHLNDVAKRTEKSDVSPFVYVIMAFRANKPEYENALICEQOLIMC 240
 DB 181 GTAKNGGCTIYMAEHLNDVAKRTEKSDVSPFVYVIMAFRANKPEYENALICEQOLIMC 240
 QY 241 IKSNGRPVDDITEYCPREIISLMKLCWEANPEARPTFGIIEKRPFLISOLESVED 300
 DB 241 IKSNGRPVDDITEYCPREIISLMKLCWEANPEARPTFGIIEKRPFLISOLESVED 300
 QY 241 IKSNGRPVDDITEYCPREIISLMKLCWEANPEARPTFGIIEKRPFLISOLESVED 300
 DB 241 IKSNGRPVDDITEYCPREIISLMKLCWEANPEARPTFGIIEKRPFLISOLESVED 300
 QY 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEQPSLSHSSQGLGMGPVEESMFA 360
 DB 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEQPSLSHSSQGLGMGPVEESMFA 360
 QY 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEQPSLSHSSQGLGMGPVEESMFA 360
 DB 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEQPSLSHSSQGLGMGPVEESMFA 360
 QY 361 PSLEHPOENEPSLOSRLQDEANVHLVYSSRMDRQKQPRONVAVNREERRRVSHPDF 420
 DB 361 PSLEHPOENEPSLOSRLQDEANVHLVYSSRMDRQKQPRONVAVNREERRRVSHPDF 420
 QY 361 PSLEHPOENEPSLOSRLQDEANVHLVYSSRMDRQKQPRONVAVNREERRRVSHPDF 420
 DB 361 PSLEHPOENEPSLOSRLQDEANVHLVYSSRMDRQKQPRONVAVNREERRRVSHPDF 420
 QY 421 AQQRPYENFQNTTEGKGVYSSAASHGNVHOPSGILTSOPVLYONNGLYSSHGFEETPLD 480
 DB 421 AQQRPYENFQNTTEGKGVYSSAASHGNVHOPSGILTSOPVLYONNGLYSSHGFEETPLD 480
 QY 421 AQQRPYENFQNTTEGKGVYSSAASHGNVHOPSGILTSOPVLYONNGLYSSHGFEETPLD 480
 DB 421 AQQRPYENFQNTTEGKGVYSSAASHGNVHOPSGILTSOPVLYONNGLYSSHGFEETPLD 480
 QY 481 PGTAGPRVWYRPIPSHMSLHNIPVETNYLGNTPTMPFSSLPPTDESIKTYIYNSTGIQ 540
 DB 481 PGTAGPRVWYRPIPSHMSLHNIPVETNYLGNTPTMPFSSLPPTDESIKTYIYNSTGIQ 540
 QY 481 PGTAGPRVWYRPIPSHMSLHNIPVETNYLGNTPTMPFSSLPPTDESIKTYIYNSTGIQ 540
 DB 481 PGTAGPRVWYRPIPSHMSLHNIPVETNYLGNTPTMPFSSLPPTDESIKTYIYNSTGIQ 540
 QY 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYOALFNDTITSLDKHDPIDENIGKHMKN 600
 DB 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYOALFNDTITSLDKHDPIDENIGKHMKN 600
 QY 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYOALFNDTITSLDKHDPIDENIGKHMKN 600
 DB 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYOALFNDTITSLDKHDPIDENIGKHMKN 600
 QY 601 CARLIGTQSOIDSIDHDYERDGLKEKYOMLQKWMVMEGIGKATVGLAALHQCSDID 660
 DB 601 CARLIGTQSOIDSIDHDYERDGLKEKYOMLQKWMVMEGIGKATVGLAALHQCSDID 660
 QY 601 CARLIGTQSOIDSIDHDYERDGLKEKYOMLQKWMVMEGIGKATVGLAALHQCSDID 660
 DB 601 CARLIGTQSOIDSIDHDYERDGLKEKYOMLQKWMVMEGIGKATVGLAALHQCSDID 660
 QY 661 LLSLLIYVSON 671
 DB 661 LLSLLIYVSON 671

RESULT 2
 ID RIK1_MOUSE STANDARD; PRT; 656 AA.
 AC Q06855;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.-)
 DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)
 DE (Receptor interacting protein).
 GN RIP1 OR RIP OR RINP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=95277838; PubMed=7538908;
 RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.
 RT "RIP: a novel protein containing a death domain that interacts with Fas/Apo-1 (CD95) in yeast and causes cell death."
 RL Cell 81:513-523(1995).

- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFR1 IN A TNF-DEPENDENT PROCESS. REQUIRED FOR TNFR1 ACTIVATION OF NF-KAPPA B.
 - TISSUE SPECIFICITY: FOUND AT LOW LEVELS IN ALL TISSUES.
 - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 - SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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EMBL: U25995; AB060487.1; -.
 DR HSSP: P25445; 1DPE.
 DR MGD: MGI:108212; Ripk1.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00531; death; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00221; STYKC; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding; Apoptosis.
 KW Apoptosis.
 FT DOMAIN 17 290
 FT NP_BIND 23 31
 FT BINDING 49 49
 FT ACT_SITE 138 138
 FT DOMAIN 583 669
 FT VARIANT 473 473
 FT SEQUENCE 656 AA: 74854 MW: AB0350B523879933 CRC64;

Query Match 68.4%; Score 2423.5; DB 1; Length 656;
 Best Local Similarity 69.8%; Pred. No. 1.7e-135;
 Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

QY 1 MOPDMSLVINIKKSSDFLESALDSGGFGKVSICFHRTOGLIMIKTVYKGPNCIEHNEAL 60
 DB 1 MOPDMSLVINIKKSSDFLESALDSGGFGKVSICFHRTOGLIMIKTVYKGPNCIEHNEAL 60

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OY 61 LEAKMMNRHSHRVKLLGYIEGKYSLYMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
DB 61 LEEKMMNRHSHRVKLLGYIEGKYSLYMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
OY 121 EIEGMCYLHGKGYIHKDLKPEKNTLVNDPHIKIADGLASFCKMSKLNNEEHLREVD 180
DB 121 EIEGMCYLHGKGYIHKDLKPEKNTLVNDPHIKIADGLASFCKMSKLNNEEHLREVD 180
OY 181 GTAKK-NGTLYYMAPEHLNDVNAKPEKSDVYSFAVVLMAIFANKPEYENALCEQQLIM 239
DB 181 STKKNNGGTLXYMAPEHLNDVNAKPEKSDVYSFAVVLMAIFANKPEYENALCEQQLIM 240
OY 240 CIKSGNRPVDDITYECPREILSLMKUCMEANPEKPPFPGIEEKREFFYSQLEESVEE 299
DB 241 CIKSGNRPVDDITYECPREILSLMKUCMEANPEKPPFPGIEEKREFFYSQLEESVEE 300
OY 300 DVKSLKREYSNENAVKRMOSLQDCVAVPSRSNSATDEQSGLSHSGGLMGPEEESWF 359
DB 301 DVASLKREYSPQSVLQRMESLQDCVAVPLPSRSNS--EQPGSLSHSGGLMGPEEESWF 358
OY 360 APSLEHPOENEPSLOSRLQDEANVHLGSHMDROTQKOPRONVAYNNEEERRRRSHDP 419
DB 359 SSPEYPODENRDSVQAKLOEASVHAFGIFAEKOTKQPRQNEAYNNEEERRRRSHDP 418
OY 420 FAQGRPEENFQNTGKGTIVSSAASHGNVHQPGLTSQPOVLYONNGLYSHGFTPL 479
DB 419 FAQGRPEENFQNTGKGTIVSSAASHGNVHQPGLTSQPOVLYONNGLYSHGFTPL 470
OY 480 DPGTAGRPVWRPPIPSHMPSLHNPVPEKNTLVNDPHIKIADGLASFCKMSKLNNEEHLREVD 539
DB 471 --GTTGGVWYPPMLSQSYSTYKPPVPEKNTLVNDPHIKIADGLASFCKMSKLNNEEHLREVD 528
OY 540 QIGAVNYMEIGTSSSLDSTNTNFKPEPAKYOAFIENNTSLDKHLDPIRENLGKHWK 599
DB 529 QIGHNNTMDVGLN---QPPNNTCKEESTSRHQAIFENNTSLDEHNLPRENLGKHWK 584
OY 600 NCARKLGFTQSQIDEIDHDERDGLKEKRYOMLQKVMREKIGATYVGLKLAQALHQCRI 659
DB 585 NCARKLGFTQSQIDEIDHDERDGLKEKRYOMLQKVMREKIGATYVGLKLAQALHQCRI 644
OY 660 DLSSLIYVSON 671
DB 645 DLNHLIRASOS 656

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RESULT 3

RIP3_HUMAN

STANDARD; PRT; 518 AA.

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AC 09Y572;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 3 (EC 2.7.1.1.-)
DE (RIP-like protein kinase 3) (Receptor-Interacting protein 3) (RIP-3).
GN RIP3 OR Rip3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-50.
RC TISSUE=Cervical carcinoma, and lymphocytes;
RX MEDLINE=992872740; PubMed=10339433;
RA Yu P.W., Huang B.C.B., Shen M., Quast J., Chan E., Xu X., Nolan G.P.,
RA Payan D.G., Luo Y.,
RT "Identification of RIP3, a RIP-like kinase that activates apoptosis
RT and NFkappaB."
RL Curr. Biol. 9:539-542(1999).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-50.
RC TISSUE=Fetal brain, and Aortic endothelium;
RX MEDLINE=99287880; PubMed=10358032;
RA Sun X., Lee J., Navas T., Baldwin D.T., Stewart T.A., Dixit V.M.;

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RT "RIP3, a novel apoptosis-inducing kinase.";
RL J. Biol. Chem. 274:16871-16875(1999).
CC -1- FUNCTION: Promotes apoptosis.
CC -1- SUBUNIT: Binds TRAF2 and RIPK1 and is recruited to the TNFR-1
CC signaling complex.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: Highly expressed in the pancreas. Detected at
CC lower levels in heart, placenta, lung and kidney.
CC -1- PTM: Autophosphorylated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
CC EMBL; AF156884; AAD39005.1; -
CC Genew; HGNC:10021; RIP3.
DR InterPro; IPR000719; Euk_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation; Apoptosis.
FT DOMAIN 21 287
FT NP_BIND 27 35 ATP (By similarity).
FT BINDING 50 50
FT ACT_SITE 142 142 BY SIMILARITY.
FT MUTAGEN K->A: ABOLISHES KINASE ACTIVITY.
FT MUTAGEN 50 50 K->D: ABOLISHES KINASE ACTIVITY.
SQ SEQUENCE 518 AA; 56901 MW; 38A3ECFBBBD4151 CnC64;
Query Match 11.9%; Score 423; DB 1; Length 518;
Best Local Similarity 25.3%; Pred. No. 6.9e-18;
Matches 145; Conservative 95; Mismatches 186; Indels 146; Gaps 22;
OY 14 SSDFLESSEL-DSCGFVKSLCFHRTQGLIMTKYKPCNCEHNEALFEAKMNRHRH 72
DB 17 STEELNELVKGKQGFVFRQHRKKG-----YDAVAVIVSKAISREYKAMASIDN 69
OY 73 SRVYKLLGVI-----IEGKYSLYMEYMEKGNLMHVLKAEKSTPLSVKGRILLIEGMC 127
DB 70 EFLVRLKEGVIEKVMNDQPKPALVTKFMENGLSLGLOSQCPRPWPLLCRLKEVYLGMF 129
OY 128 YLHGKG--VHKDLKPEKNTLVNDPHIKIADGLASFCKMSKLNNEEHLREVDGTRAK- 184
DB 130 YLHQNPLVLRHDKLPNSVLPDPDLHVLAFLGSLTFQGSQ-----SGTCSG 177
OY 185 KNGGILYMAPEHLNDVNAKPEKSDVYSFAVVLMAIFANK-----PYE-----NAICEQ 236
DB 178 EPGGLGLYLAPELFLVNNVNRKASTASDVYSFGLKMAVLAAGREVELPTEPSLYAEVACRQ 237
OY 237 LIMCIRKSNRPVDDITYECPRE-----IISLMKLCMEANPEKPPFPGIEEKRRP 287
DB 238 -----NRSLSLAEPLQAGPEFTGLGKRLKMLQWCSSEKDKRPSQECLEPKTDEVYQ- 288
OY 288 FYLSQLEESVEDYSLKKEYSNENAVKRMOSLQDCVAVPSRSNSATDEQSGLSHSG 347
DB 289 -----MVENNNMAASTVYDFLSQLKSSNRPE-----SIPES----- 320
OY 348 GLGMCVPEESWFAFSLHPOENEPSLOSRLQDEANVHLGSHMDROTQKOPRONVAYNR 407
DB 321 --GOGGTMDGFRRTIENQHSRNDVWVSEWL-----NKLLEPSPSSVPAKC 365
OY 408 EE-ERRRRVSHDPAQORPYENFQNTGKGTIVSSAASHGNVHQPGLTSQPOVLYONN 466

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[illegible]

Db	14	ISLVGSEEDLNLFVCGKGFVAFRRARHTAMNLDVAVK-----IYNSKISREYKAMV	66
OY	69	RLRRSRVYKLLGVITIE-EGKY-----SLVWVEYMEKGLMHVYKAEKSTPLSYKGRILLETI	122
Db	67	NLRNENVALLLLGSTENLEMDIYVGPALVGFENMESLSGLLOSCPSPWPLLCRLLEVV	126
OY	124	EGCMYLLH--GKGYIHKDKLENILVYNDPHIKIADGLASFEMKSKLNNEEHNELREVDG	181
Db	127	LCGMYLIHSLNPILLHRDKRQSNVLLDLELHAFLADFGISTFGGSSQSSS-----GS	177
OY	182	TAKNNGSTILYMAPEHLDVNMNAKPTLEKSVYSFAVYLAAILANKPE-----YENAIIC	233
Db	178	GSRSRGSTILYLAPE--LLNDGKASKASDVYSFGVLTWTVLAGREAEVVDKTSILRGAVC	236
OY	234	EOQLIMICIKSGNPDVDDITREYCPRE-----IISIMKLCWEANPEARPTFGIEKPRPF	288
Db	237	NRQ-----RRPLELTELPRDPSPELFGLEGKELMTICHSSEPKDRSPFODCSKTNV	286
OY	289	YLISOLEESVEEDYKSLK---KEYSNENAVYKRMOSLO---LDCAVAPSSKSNATBOPG	341
Db	289	YI--IYVDKRYVAASVKYKHYLSQYRSSDPTKLSARESSQKGTEDVC-----PRETIYEMLD	344
OY	342	SLHSQSGLGVPVEESMFAPSLIEHPDEHEPRLQSKLDDEANYHLYGSRMDRQIKQCPRQ	401
Db	343	RLH-----LEEPS-----GSPERLITSL-----	360
OY	402	NVAYNREERERRRVSHPDPAOQRPVENFONTEGKGTIVYSASASHGNVAHQPSGLTSSO---	458
Db	361	-----TERRG-----KEASFGHAH--PAGISSDTPLA	384
OY	459	--POVLQYNNGLKSSHGFGTGPLDDEGTAGPRWYKPIFISHMPSLHNIIVPETN-----	509
Db	385	GTPQIPH---TLPSSGTTTPPAFTETPPSD-----PDRNGDGRNS	422
OY	510	---YLNGTPTMPSPSSLPPTDESIKYITVNSTGIQIGAVNMEIGTSSSLDSTNTNF-K	565
Db	423	NPWYTWMAPI--PATGL-----GSI--VLNCCSVOIGQINCMNV-----QPRTAIFPK	466
OY	566	EEPA 569	
Db	467	KEPA 470	
RESULT 5			
RIK3_MOUSE	ID	RIK3_MOUSE	STANDARD; PRT: 486 AA.
AC	O9QZL0;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Receptor-interacting serine/threonine protein kinase 3 (EC 2.7.1.1-)		
DE	(RIP-like protein kinase 3) (Receptor-interacting protein 3) (RIP-3)		
DE	(mRIP3).		
GN	RIPK3 OR RIP3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-143.		
RC	TISSUE=Embryo;		
RX	MEDLINE=99421935; PubMed=10490590;		
RA	Pazdernik N.J., Donner D.B., Goebel M.G., Harrington M.A.;		
RT	"Mouse receptor interacting protein 3 does not contain a caspase-		
RT	recruiting or a death domain" but induces apoptosis and activates NF-		
RT	kappaab.";		
RL	Mol. Cell. Biol. 19:6500-6508(1999).		
CC	-1- FUNCTION: Promotes apoptosis.		
CC	-1- SUBUNIT: Binds TRAF2 and RIPK1 and is recruited to the TNFR-1		
CC	signaling complex (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).		
CC	-1- TISSUE SPECIFICITY: Expressed in embryo and in adult spleen,		
CC	liver, testis, heart, brain and lung.		

	-1	PIM: Autophosphorylated.
CC	-1	SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC		
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CC		
DR		EMBL; AF178953; AAF03133.1; -
DR	MGP:	MGI:2154952; RPK3.
DR	InterPro;	IPIR000719; Euk_kinase.
DR	InterPro;	IPIR002290; Ser_thr_kinase.
DR	pfam;	PF00069; Pkinase; 1.
DR	PRINTS;	PR00109; TYKINASE.
DR	PROSITE;	PS00107; PROTEIN_KINASE_ATP_1.
DR	PROSITE;	PS00108; PROTEIN_KINASE_ST_1.
DR	PROSITE;	PS50011; PROTEIN_KINASE_DOM_1.
RW		Transferrase; Serine/threonine-protein kinase; ATP-binding; phosphorylation; Apoptosis.
KW	DOMAIN	22 292
FT	NP_BIND	28 36
FT	BINDING	51 51
FT	ACT_SITE	143 143
FT	DOMAIN	352 438
FT	MUTAGEN	143 143 D->N: NO AUTOPHOSPHORYLTATION.
FT	SEQUENCE	486 AA; 53336 MW; DD264E6918703436 CnC6d;
Query Match	11.3%; Score 401.5; DB 1; Length 486;	
Best Local Similarity	24.8%; Pred. No.1.2e-16;	
Matches 150; Conservative 87; Mismatches 191; Indels 177; Gaps 23;		
OY	8 NVIKMKSDFLESAE-LDSGFGVGLCFHFHTQGLMIKKTYKPCNEHNALLEEKMM	66
Db	12 SAVPLVSHEELKLIEFVGKGSGGVGFRAHHRTMHDAVK-----IVNSKKLSWEKYA	64
OY	67 MNRLRHSHVVLLGVIIIEEGRY-----SLVMYEKEGNLMHVLAENSTPLSVGRITL	120
Db	65 MVNLRENVALLLDGY-FEDLGWDPEVSQALVTREMENSAGLIQLDECPRPWPILLRIQLQ	123
OY	121 EIISGCYLHG-KGVTHDKLPENILDNDFHIXIADVLGIASFRRMSKLNNEBHETIRE	178
Db	124 EVVLGMCTYHLDPLLRDLKPENIIDPLPAHLAKLDFGLSTFOGSGSGSGSGSRD	183
OY	179 VDGTRAKNGGFLYYMAPRHLMDVAAPLKESGDVYSFAVVIWAIFANKPP-----YEN	230
Db	184 -----SGGTATLVDPELLERKYNMLKASKADVSYFGLLVAAVLAGEAEIDVKTSLIRE	236
OY	231 AIICEOOLIMCKSGNRPDVIDITEYCP----RETISIIMKCMEANPARPTPGIEKEF	285
Db	237 TVCDRO-----SRPLLTLPLPGSPETPBLETIKELMTIHMGQSQSENRSFDODEPXT	288
OY	286 RPFLISOLESEVEDVDSLKEYSNENAAYVRMOSLOLDCAAVPSRSNSATEOGSLHS	345
Db	289 NEVY-NLVKDDVDAVSEVKHYLSQ-----HR	314
OY	346 SOGLGMGEVSWARPASLEHQENEPSSLOSXLDEANTHLXGSAMDROTQQORONVAY	405
Db	315 SSGRNLSAREPSOKOTENDCPRE---TWWSKM-----LDLHLHPESPYPGG	358
OY	406 NREEERR-----RVSHDPFAAQRPENFONTGCKGVNYSSASHGNNAVHQPGL	455
Db	359 KCPERQAODTSYGATPAKTTSDPYA-----GT-----	386
OY	456 TSQOVLYQNNGLYSSHGFGTPRLDPCGTAAGRMYWRIPISHMPISLNIHVEPNY--LG	512
Db	387 ---PQI-----PTHLPFRGTGT-----PVTFETHPGPH---PQRNQDGGRH	421
OY	513 NTPEPMRESSLPPTDESIRYTIYTNSTGIOGAANYHMEIGCTSSSLIDSTNTNFKEBPARY	572

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Db      422  GTPWTPMTPPMPNPGPALVFNNSQVIGSNYN-----SLVAPPRTT--ASSSAKY 470
QY      573  -QAIF 576
          ||
Db      471  DOAOF 475

RESULT 6
ID      RIK2_MOUSE
AC      P58801;
DT      15-JUN-2002 (Rel. 41, Created)
DT      15-JUN-2002 (Rel. 41, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.-).
GN      RIKP2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6;
RX      MEDLINE=21891093; PubMed=11894097;
RA      Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
RT      "Involvement of receptor-interacting protein 2 in innate and adaptive
RT      immune responses."
RL      Nature 416:190-194(2002).
CC      -i- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC      CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity).
CC      -i- SUBUNIT: Binds to CELAR/CLAP and CASP1 via their CARD domains.
CC      Binds to BIRC3/-IAP1 and BIRC2/C-IAP2, TRAF1, TRAF2, TRAF3 and
CC      TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC      receptor complex (By similarity).
CC      -i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -i- PTM: Autophosphorylated (By similarity).
CC      -i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      -i- SIMILARITY: CONTAINS 1 CARD DOMAIN.
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Cc      or send an email to license@isb-sib.ch).
Cc      -----
Cc      EMBL, AF461040; AAL96436.1;
Cc      DR PROSITE: PS50209; CARD. 1.
Cc      DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
Cc      DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
Cc      DR PROSITE: PS00108; PROTEIN_KINASE_ST. 1.
Cc      KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
Cc      FT Phosphorylation; Apoptosis.
Cc      FT DOMAIN 18 294 PROTEIN_KINASE.
Cc      FT DOMAIN 431 523 CARD.
Cc      FT NP_BIND 24 32 ATP (By similarity).
Cc      FT BINDING 47 47 ATP (By similarity).
Cc      FT ACT_SITE 146 146 BY SIMILARITY.
Cc      SQ SEQUENCE 539 AA: 60400 MM; 42951BF9CA15DFA CRC64;

Query Match * 10.6%; Score 374; DB 1; Length 539;
Best local similarity 30.0%; Pred. No. 5,66-15;
Matches 100; Conservative 67; Mismatches 126; Indels 40; Gaps 10;

QY      55  EHNEALLIEEAKMMNRRLSHRSVYKLLGVITIEGKYSLVMEYKEGKNLHVIAKENSTP-- 111
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      59  ERND-ILREAEILHKARFSYILPLTIGCNEPEFGIATEYWPMSGNELDLHREKTEYDIA 117

QY      112 LSVGRITLLEIEEGCYLHGKG--VIRKDLKPEINLVNDNFHITADGLASFMMWSKLN 169
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      118 WPLRRILHETALGVNTHNNNPPLLDLDTQNIILDNDEHVAIVADFGLSKRWMSLSLO 177

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OY 170 NEHNELREVDGTAKNGGTLTYAPAEHLNDVNAKPTKRS-----DYVSAFVAVLMAIFA 223
D6 178 SRSYKSAPE-----GGTIIYMPPE-----NYPEGKSRASVYKHDIYSYAVIMWEVLS 224
OY 224 NKEPEENACIEQOLIMCISGNRPVDDITECPREI-----ISLMKICWENPAREPT 277
D6 225 RKQPEEYVNTQIMYSVQGRPTPSE--ENLPEDIPHRGIMISLISQGMQONDERRS 282
OY 278 FPGIEKRPREFYLSQLESVEDVYSLKKEYSNEAVKRMQSLQLD-CVAVSSRSNSA 336
D6 283 FLKCLIELEPVLRITPREDITFLEAVYQLKKAKIQSSSTIHLCDKMDLSLNPANHPPE 342
OY 337 TEQPEGLSHSQGLGMPVEESWFAPSLHPQEE 369
D6 343 ESCGSSLLSRMTGSPGP-----SRSLSAPODK 369

RESULT 7
RIR2_HUMAN
ID RIR2_HUMAN STANDARD: PRT; 540 AA.
AC Q4353;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 (BC 2.7.1.-)
DE (RIP-2) (CARD-containing interleukin-1 beta converting enzyme
DE associated kinase) (CARD-containing IL-1 beta ICE-kinase).
DE RIPK2 OR RICK OR RIP2 OR CARDIAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
[1]
RN RP MEDLINE=98241596; PubMed=9575181.
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
RT "RICK, a novel protein kinase containing a caspase recruitment domain,
RT interacts with CLARP and regulates CD95-mediated apoptosis.";
RL J. Biol. Chem. 273:12296-12300(1998).
[2]
RN RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RA MEDLINE=98241596; PubMed=9575181.
RT "Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
RT RICK, a novel protein kinase containing a caspase recruitment domain,
RT interacts with CLARP and regulates CD95-mediated apoptosis.";
RL J. Biol. Chem. 273:12296-12300(1998).
[3]
RN RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RA MEDLINE=98381580; PubMed=9705938;
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
RA Mattmann C., Tschopp J.;
RT "Identification of CARDIAK, a RIP-like kinase that associates with
RT caspase-1.";
RL Curr. Biol. 8:885-888(1998).
[4]
RN RP SEQUENCE FROM N.A.
RA Ozersky P., Holmes A., Brox M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[5]
RN RP SEQUENCE FROM N.A.
RA Platzner M., Varon R.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[6]
RN RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB.
CC -1- SUBUNIT: Binds to CLARP/CLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and
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CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,
CC peritoneal blood leukocytes, spleen, kidney, testis, prostate,
CC pancreas and lymph node.
CC -1- PTM: Autophosphorylated.
CC -1- SIMILARITY: BELONGS TO THE SER/TRP FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL, AF027706; AAC34970.1; -
DR EMBL, AF078530; AAC27722.1; -
DR EMBL, AF064824; AAC25668.1; -
DR EMBL, AC004003; AAC24561.1; -
DR EMBL, AF117829; AAD04634.1; -
DR EMBL, BC004553; AAH04553.1; -
DR Genew; HGNC:10020; RIPK2.
DR MIM; 603455; -
DR InterPro: IPR001315; CARD.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transfaser; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 18 294 PROTEIN KINASE.
FT DOMAIN 432 524 CARD.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP.
FT ACT_SITE 146 146
FT MUTAGEN 47 47 K->A: ABOLISHES KINASE ACTIVITY.
FT MUTAGEN 146 146 K->M: REDUCES PAS-MEDIATED APOPTOSIS.
FT MUTAGEN 146 146 D->N: ABOLISHES KINASE ACTIVITY.
SQ SEQUENCE 540 AA: 61194 MW; 575A692339505792 CRC64;

Query Match 10.5%; Score 371; DB 1; Length 540;
Best Local Similarity 28.8%; Pred. No. 8.4e-15;
Matches 112; Conservative 68; Mismatches 145; Indels 64; Gaps 12;

OY 23 LDSGFGKVSICFH--RTQGLIMTKTYKGPNCIEHNEALLERAKMNRRLRHSRYVKL 79
D6 24 LSRGASGVSSARRADRWQ-VAVKHLIHHPLLDSEKRDVLRBAEILHKRKFYILPIL 82
OY 80 GVITIEGYSLVMEYMEGNLMLHLKAKMSTP--LSYKGLIIEITIEGKYLHG--KGV 134
D6 83 GICNEPEFLGIVTEYMPGSLNELIHRTEXPDVAMPPLRIELHIALGVYVLIHNMPP 142
OY 135 IAKDLKPENLIVNDGFHIKIDGLASFPMKSKLNNEHNLREVDGTAKNGGTLTYMA 194
D6 143 LHHDLKQNIILLNDEFHVKINDPGLSKRMMSLSQSSKSAPE-----GGTIIYMP 194
OY 195 PEHLNDVNAKPTKRS-----DYVSAFVAVLMAIFANKEPEYNAICQOLIMCISGNRP 248
D6 195 PE-----NYPEGKSRASIKRDIYSYAVITWEVLSRQPFEDVNNPIQIMYSVQGRPV 249
OY 249 VDDITECPREI-----ISLMKICWENPAREPTFPGIEKRPFFYLSQLESVEDVK 302
D6 250 INE--ESLPVDIPRRARMTSLIESGMQONPDERPSFLKCLTELEPVLRITFLEAVI 307
```

DR	SMART: SMO0248; ANK_10.
DR	SMART: SMO0221; STYKC_1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST_1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM_1.
DR	PROSITE; PS50297; ANK_REPEAT_REGION_1.
DR	PROSITE; PS50088; ANK_REPEAT_9.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW	ANK repeat; Alternative splicing.
FT	DOMAIN 22 286 PROTEIN KINASE.
FT	REPEAT 485 514 ANK 1.
FT	REPEAT 518 547 ANK 2.
FT	REPEAT 551 580 ANK 3.
FT	REPEAT 584 613 ANK 4.
FT	REPEAT 617 647 ANK 5.
FT	REPEAT 651 680 ANK 6.
FT	REPEAT 684 713 ANK 7.
FT	REPEAT 717 746 ANK 8.
FT	REPEAT 750 780 ANK 9.
FT	REPEAT 782 811 ANK 10.
FT	NP_BIND 28 36 ATP (BY SIMILARITY).
FT	ACT_SITE 143 143 ATP (BY SIMILARITY).
FT	VARSPLIT 278 325 BY SIMILARITY.
FT	CONFLICT 714 714 MISSING (IN ISOFORM 2).
SO	SEQUENCE 832 AA; 91610 MW; 5D8FFD5F04FE7EBC CRC64;
Query Match	10.5%; Score 370.5; DB 1; Length 832;
Best Local Similarity	28.2%; Pred. No. 1.6e-14;
Matches 128; Conservative	70; Mismatches 167; Indels 89; Gaps 18;
QY	14 SSDFLSAELDSGSGFGKVSCLCFHRFGGLMIKT--VYKGNC-IENNE-ALLEAKKM 67 : : : : : : : : : : : :
Dd	19 AGEFTGWKEKVGSGCGFYGVKYRH-----VHKMTLAIKCSPLHYDDREFMELLEAKKM 73 :
QY	68 NRLHSNRVKKLVITIEEGKSIVMETWEKNLMHLVKAEMSTPLSKVGRILLIETIGMC 127 : : : : : : : : : : : : : : : : : :
Dd	74 EMAKFRRYLIPVYGICRE--PYGLVMETWEKTSLEKLASE-PLPWDLRFRIIHETAVGMN 130 : : : : : : : : : : : : : : : : : :
QY	128 YLH--GKGVIHKADPENIIIVDNDFHIKIADLGASFMMMSKLNNEEHNELREVDTAAK 185 : : : : : : : : : : : : : : : :
Dd	131 FLHCMAAPRLHLIDKPANIILLDAIRHYKISDFGLA-----KCNGLSHSLSDGLF-- 182 :
QY	186 NGSTLYYMAPRHLNDVNAKPTKESDVYSFAVLVAIFANKPEYNALICEQOLIMCISGN 245 : : : : : : : : : : : : : : : : : :
Dd	183 --GTIAVLPERRIKERSRLFOTKHHDVYSFALIVGVLTKQKPFADERNILHIVKVYGH 240 :
QY	246 RPVDVDITEYPR--ELISMKLCEWENPARTF----- 278 : : : : : : : : : : : : : : : : : :
Dd	241 RPELRPCVRARPRACSHLIRLMOCWOGDPFRVPTFGNGINGELIROVLALLPVYGRW 300 : : : : : : : : : : : : : : : : : :
QY	279 --PGIEEKFR-----PFLSOLFEEVEEDVYSLKKEYSNENAVVRMGSLDLC 325 : : : : : : : : : : : : : : : : : :
Dd	301 RSPG--EGFRLESEVIIRVTCPLSSPOEITSETDLCEKPDDEVKETR-----HDDL 351 : : : : : : : : : : : : : : : : : :
QY	326 VAVPSRSKN-----SATQDGSLHSSOGLMGVYESMFAPSLEHPQENEPSLOS 376 : : : : : : : : : : : : : : : : : :
Dd	352 KSPEEPSEEVYPARKLRASAPTENDYSLSELISQ--LDGSGVAGVGEPELSRSSSES 408 : : : : : : : : : : : : : : : : : :
QY	377 KLQDE-ANYHLYG--SRMDROTQQPPRONVAYNRE 408 : : : : : : : : : : : : : : : : : :
Dd	409 KLPSGGSGKRLLSGVSYSDSAFSRGSLSEERE 442 : : : : : : : : : : : : : : : : : :
RESULT 9	
ID	TGIR_HUMAN STANDARD; PRT; 1367 AA.
AC	P08069;
DT	01-AUG-1988 (Rel. 08, Created)
DT	01-AUG-1988 (Rel. 08, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Insulin-like growth factor I receptor precursor (EC 2.7.1.112) (CD221 antigen).

GN IGFLR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=87053815; PubMed=2877871;
 RA Ullrich A., Gray A., Tam A.W., Yang-Peng T., Teubokawa M.,
 RA Collins C., Henzel W., Bon T.L., Kothur S., Chen E., Jacobs S.,
 RA Francke U., Ramachandran J., Fujita-Yamaguchi Y.,
 RT "Insulin-like growth factor I receptor primary structure: comparison
 RT with insulin receptor suggests structural determinants that define
 RT functional specificity.";
 RL EMBO J. 5:2503-2512(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92268129; PubMed=1316909;
 RA Abbot A.M., Bueno R., Pedrini M.T., Murray J.M., Smith R.J.,
 RT "Insulin-like growth factor I receptor gene structure.";
 RL J. Biol. Chem. 267:10759-10763(1992).
 RN [3]
 RP SEQUENCE OF 1-31 FROM N.A.
 RX MEDLINE=91282751; PubMed=1711844;
 RA Cooke D.W., Bankert L.A., Roberts C.T. Jr., Lerolth D.,
 RT Casella S.J.,
 RT "Analysis of the human type I insulin-like growth factor receptor
 RT promoter region.";
 RL Biochem. Biophys. Res. Commun. 177:1113-1120(1991).
 RN [4]
 RP SEQUENCE OF 1137-1193 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Melanocyte;
 RX MEDLINE=94067791; PubMed=8247543;
 RA Lee S.-T., Strunk K.M., Spritz R.A.,
 RT "A survey of protein kinase mRNA expressed in normal human
 RT melanocytes.";
 RL Oncogene 8:3403-3410(1993).
 CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
 CC WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
 CC TYROSINE-PROTEIN KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE
 CC BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-
 CC BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
 CC RECEPTOR SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL: X04434; CAA28030.1; -;
 DR EMBL: M69229; AAB59399.1; -;
 DR PIR: A25690; A25690.
 DR HSSP: P06213; IIRK.
 DR Genew: HGNC:5465; IGFLR.
 DR MIM: 147370; -;
 DR InterPro: IPR000494; EGFR_L_domain.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR002174; Furin-like.
 DR InterPro: IPR002011; RTkinaseI.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00041; fn3; 2.

DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00757; Furin-like; 1.
 DR Pfam: PF01030; Recep_L_domain; 2.
 DR PRINTS: PR0109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00060; FN3; 3.
 DR SMART: SM00261; FU; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR TRANSFERASE: TYROSINE-PROTEIN KINASE; Receptor; Transmembrane;
 KW Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 740
 FT FT
 FT CHAIN 741 1367
 FT FT
 FT DOMAIN 741 935
 FT TRANSMEM 936 959
 FT FT
 FT DOMAIN 960 1367
 FT FT
 FT DOMAIN 607 828
 FT DOMAIN 829 1274
 FT NP_BIND 1005 1013
 FT BINDING 1033 1033
 FT ACT_SITE 1135 1135
 FT DISULFID 215 224
 FT DISULFID 219 230
 FT DISULFID 231 239
 FT DISULFID 235 248
 FT DISULFID 251 260
 FT DISULFID 264 276
 FT DISULFID 282 303
 FT DISULFID 307 321
 FT DISULFID 324 328
 FT CARBOHYD 51 51
 FT CARBOHYD 102 102
 FT CARBOHYD 135 135
 FT CARBOHYD 244 244
 FT CARBOHYD 314 314
 FT CARBOHYD 417 417
 FT CARBOHYD 438 438
 FT CARBOHYD 534 534
 FT CARBOHYD 607 607
 FT CARBOHYD 622 622
 FT CARBOHYD 640 640
 FT CARBOHYD 747 747
 FT CARBOHYD 756 756
 FT CARBOHYD 764 764
 FT CARBOHYD 900 900
 FT CARBOHYD 913 913
 FT MOD_RES 1165 1165
 FT SEQUENCE 1367 AA; 154792 MW; A68A735F87F745C8 CRC64;
 Query Match 9.8%; Score 346.5; DB 1; Length 1367;
 Best Local Similarity 27.9%; Pred. No. 8.3e-13;
 Matches 117; Conservative 64; Mismatches 147; Indels 91; Gaps 18;
 QY 20 SAELDSGSGFGRV-----SLCFHRTGIMIMKTYKSPNCIEHNEALLLEAKMMNRRLRS 73
 DB 1002 SRELGGSGFGMYGVGAKGVKDEPRVAIKTYVNEAASMRERIE-FLNEASVYKKEKNCH 1060
 QY 74 RYVALLGVIIIEGKYSLYMEYMEKGNL--MHVLAKAAMS-----TPLSVKGRIIL--EIT 123
 DB 1061 HYVALLGVSVSGQPTLVIMELMTRGDLKSYLSRSLRPENNPNVPLAPSLSKMIOAGEIA 1120
 QY 124 EGMCTYLGKGVYIHDLPENILVNDPHIKIADIGLASFKMWSKLNNHEINELREVDCIA 163
 DB 1121 DGMAYVLANKFVHMDLARKMCVAEDFTVKIGDGM-----RDYEYDYR 1167
 QY 184 KKNKGTL--YYMADEHLNDVNAKPTKSDVYSFAVVLMAIFA--NKEPYENAIQEQOLIMC 240

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DB      1168 KGGKGLPVRRMSPESLKD--GVFTTYSVWSGCVLWEIATLAEQYOGLSNEQVLRFY 1225
OY      241 IKSG--NRPDVDITFYCPREIISLMKLCMEANPEARPTFGCELEFRFPYISQLESSE 298
DB      1226 MGGGLDKPD-----NCPDMLFELMRMCWYNPKRPSFLET-----ISIKEME 1271
OY      299 EDVKSLLKREYSNENAV-----VKRQSLQDLCVAVPSSRSNATEQPSGLSHSSQGL 349
DB      1272 PGFRVSYFYSEENKLPPEPELDLPENNESVPLD-----PSASSSLPLP-DRHSGH-- 1323
OY      350 GNGVEESWPAFSLHEHQEENEPS-----LQSKLQDEANY-ILYSGRMDRQTKQOPRON 402
DB      1324 -----KAENCGPGCVLIRASFDEROPVAMHNGRKNRRLPLPOSS 1365

RESULT 10
MATK_RAT
ID      MATK_RAT      STANDARD:      PRT: 467 AA.
AC      P41243:
DT      01-FEB-1995 (Rel. 31, Last sequence)
DT      01-FEB-1995 (Rel. 31, Last annotation update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)
DE      (Tyrosine-protein kinase CTK) (Protein kinase BAKT).
GN      MATK OR CTK OR BAKT.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RC      MEDLINE=95106341; PubMed=7807586;
RA      Kuo S.S., Moran P., Grupp J., Armanini M., Phillips H.S., Goddard A.,
RA      Caras I.W.;
RT      Identification and characterization of Bakt, a predominantly brain-
RT      specific non-receptor protein tyrosine kinase related to Csk.;
RT      J. Neurosci. Res. 38:705-715(1994)
RL      J. Neurosci. Res. 38:705-715(1994)
CC      - FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION
CC      OF HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF
CC      SRC-FAMILY MEMBERS IN BRAIN.
CC      - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC      tyrosine phosphate.
CC      - SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      - TISSUE SPECIFICITY: ENRICHED IN LYMPHOID TISSUES.
CC      - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
CC      SUBFAMILY.
CC      - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC      - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: L34542; AAA64524.1; -
CC      DR      HSSP: P11362; 1FGK.
CC      DR      InterPro: IPR000719; Euk_pkinase.
CC      DR      InterPro: IPR000980; SH2.
CC      DR      InterPro: IPR001452; SH3.
CC      DR      InterPro: IPR001245; Tyr_kinase.
CC      DR      Pfam: PF00017; SH2_1.
CC      DR      Pfam: PF00018; SH3_1.
CC      DR      Pfam: PF00069; pkinase; 1.
CC      DR      PRINTS: PR00401; SH2DOMAIN.
CC      DR      ProDom: PD000001; Euk_kinase; 1.
CC      DR      ProDom: PD000093; SH2_1.
CC      DR      SMART: SM00252; SH2; 1.
CC      DR      SMART: SM00326; SH3; 1.

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DR      SMART: SM00219; TYRKc; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE: PS50001; SH2; 1.
DR      PROSITE: PS50002; SH3; 1.
KW      Transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
KW      SH3 domain; Phosphorylation.
FT      DOMAIN 22 69 SH3.
FT      DOMAIN 81 170 SH2.
FT      DOMAIN 194 443 PROTEIN_KINASE.
FT      NE_BIND 200 208 ATP (BY SIMILARITY).
FT      BINDING 221 221 ATP (BY SIMILARITY).
FT      ACT_SITE 311 311 BY SIMILARITY.
SQ      SEQUENCE 467 AA; 51896 MW; 283FF9348B5FA8F CRC64;

Query Match 9.7%; Score 343; DB 1; Length 467;
Best Local Similarity 33.2%; Pred. No. 3; Le-13;
Matches 89; Conservative 47; Mismatches 100; Indels 32; Gaps 9;

OY      21 AELDSGFGKVSICFHRQGLMT-MKTVYKGPNCIEHNEALLBEAKMMNRRLRSRYKLL 79
DB      198 AQTGESEFGAV-----LQGEYLQGVAVVAVNICKDVTQAQFDETAVMKLOHRNLVRL 251
OY      80 GVITEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKG--RIILEITGMCYLGKGVYHK 137
DB      252 GVILHHGLY-TVNEHVSKGVLNPLTRGRALVSTQSLLQFALHVAEGMETLSKLVHR 310
OY      138 DLKPENILVNDPEHRIADIGLASPKMWSKLNNEEHNEELREVDTGAKKNGTLVYAPPEH 197
DB      311 DLARNILVSEDLVAVVSDGGLAKAEKRLGLDSSRL-----PYKMTAPEA 355
OY      198 LNDVNAKPTPEKSDVYSFAVVLMAIFA-NKPEYNAICEQOLMCISGNRPVDVDTIEYC 256
DB      356 LK--NRFSSKSDVWSGCVLMEVFSYGRAPYK-MSLKREVSAYEKGVMPEPD---SC 409
OY      257 PRETISLMKLCWEPANPEARPTFGPEEK 284
DB      410 PGFVHTLMGSCWEPASRRPFRKIVEK 437

RESULT 11
IGIR_BOVIN
ID      IGIR_BOVIN      STANDARD:      PRT: 640 AA.
AC      Q05688;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Insulin-like growth factor I receptor precursor (EC 2.7.1.112)
DE      (Fragment).
GN      IGFIr.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovine; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RC      MEDLINE=92119330; PubMed=1662995;
RA      Sneyers M., Kettmann R., Massart S., Renaville R., Burry A.,
RA      Portetelle D.;
RT      Cloning and characterization of a cDNA encoding the beta-subunit of
RT      the bovine insulin-like growth factor-1 receptor.;
RT      DNA Seq. 1:405-406(1991).
CC      - FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
CC      WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
CC      TYROSINE-PROTEIN KINASE ACTIVITY.
CC      - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC      tyrosine phosphate.
CC      - SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide
CC      bonds. The alpha chains contribute to the formation of the ligand-
CC      binding domain, while the beta chain carries the kinase domain.

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CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
DR EMBL: X54980; CA38724.1; -.
DR HSSP: P06213; IIRK.
DR InterPro: IPR000719; Euk-kinase.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR002011; RTKinaseII.
DR InterPro: IPR001245; Tyr-kinase.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00069; kinase; 1.
DR ProDom: PD000001; Euk-kinase; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
DR Transfaser: Tyrosine-protein kinase; Receptor; Transmembrane;
KW Glycoprotein; ATP-binding; Phosphorylation; Repeat.
FT CHAIN 1 13
FT <1 13
FT CHAIN 14 640
FT 14 640
FT TRANSMEM 14 208
FT DOMAIN 209 232
FT DOMAIN 233 640
FT DOMAIN <1 101
FT DOMAIN 102 201
FT DOMAIN 272 547
FT NP_BIND 278 286
FT BINDING 278 306
FT ACT_SITE 408 408
FT MOD_RES 438 438
FT CARBOHYD 20 20
FT CARBOHYD 29 29
FT CARBOHYD 37 37
SQ SEQUENCE 640 AA: 72511 MW; 1E645258BDC6FEF29 CRC64;
Query Match 9.7%; Score 342.5; DB 1; Length 640;
Best Local Similarity 27.9%; Pred. No. 5e-13;
Matches 116; Conservative 67; Mismatches 148; Indels 85; Gaps 18;

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OY 20 SAELDSGGFGKY-----SLCFHRTQGLIMKTYKGCNGCTDHNALLLEAKMNRRLHS 73
DB 275 SRELGGSGFGYVESGAVGVKDEPETHVAIKTVNEASMERIE-FLNEASVMEFNC 333
OY 74 RVKLLGVYIEGKSYLVEYMEKGNL--MHVLKAEMS-----TPLSVKRIIL-ELI 123
DB 334 HVRLLGVYVSGOGLPYVMEIMETKGLSLKSLPEENNVLAAPSLSKWIMQAGETA 393
OY 124 EGMCYLHGKGVYIHKDKLENTLVNDPEFIKATDGLASFKMKSKMLNNEHNEHLEVDGTA 183
DB 394 DGMAVYLVNANKFVHDLAARNCMVAEDFVTKIGDGMT-----RDITYETDYIR 440
OY 184 KKNKGTLL--TYMAEHLNDVNAKPTKESDVSEAVVLAIFA-NKEPYENAIICQQLTMC 240
DB 441 KGGGLLPVRKMSPEISKD--GVFTTSDVWSFGVYVMEIATLAQPYQGLSNQVLAIFV 498
OY 241 IKSG--NRPDVDDITECPREIISLMKLCWANEAPPTFGIEKRPPLTSLQLESSEV 298
DB 499 MEGGLLDKPD-----NCPDMLFELMRKWCVOYNPKMRPSFLEI-----ISSVKDEME 544

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RESULT 12

ID	IGIR_RAT	STANDARD	PRT	1370 AA.
AC	P24062			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Insulin-like growth factor I receptor precursor (EC 2.7.1.112).			
GN	IGF1R			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=95277910; PubMed=7758167;			
RA	Du J., Delafontaine P.;			
RT	"Inhibition of vascular smooth muscle cell growth through antisense			
RT	transcription of a rat insulin-like growth factor I receptor cDNA.";			
RL	Circ. Res. 76:963-972(1995).			
RN	[2]			
RP	SEQUENCE OF 1-364 FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RX	MEDLINE=90017496; PubMed=2477843;			
RA	Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberis C.T. Jr.,			
RT	Leroith D.;			
RT	"Developmental regulation of the rat insulin-like growth factor I			
RT	receptor gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).			
RN	[3]			
RP	SEQUENCE OF 913-1017 FROM N.A.			
RX	MEDLINE=92412145; PubMed=1530648;			
RA	Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;			
RT	"A new member of the insulin receptor family, insulin			
RT	receptor-related receptor, is expressed preferentially in the			
RT	kidney.";			
RL	Biochem. Biophys. Res. Commun. 187:934-939(1992).			
CC	-1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)			
CC	WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A			
CC	TYROSINE-PROTEIN KINASE ACTIVITY.			
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein			
CC	tyrosine phosphate.			
CC	-1- SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide			
CC	bonds. The alpha chains contribute to the formation of the ligand-			
CC	binding domain, while the beta chain carries the kinase domain.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN			
CC	RECEPTOR SUBFAMILY.			
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC				
DR	EMBL: L29232; AAA41392.1; -.			

DR		PROSITE: PS50001; SH3; 1.	
DR		PROSITE: PS50002; SH3; 1.	
KW		Transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;	
KW		SH3 domain; Phosphorylation.	
KM		SH3	
FT	DOMAIN	58 110	
FT	DOMAIN	122 211	SH2.
FT	NP_BIND	235 482	PROTEIN KINASE.
FT	BINDING	241 249	ATP (BY SIMILARITY).
FT	ACT_SITE	262 262	ATP (BY SIMILARITY).
FT	CONFLICT	352 352	BY SIMILARITY.
FT	CONFLICT	107 108	ER -> DG (IN REF. 1).
FT	CONFLICT	400 400	MISSING (IN REF. 1).
FT	CONFLICT	466 507	ARRPRFRLAETLAEELASACAPASVSGODADGTSPPSCE P-> PASHPSANWPBSWSPGSAYGVPPPPSGRRPTVHA PKPGALTPDGGWPPQRTREVESAAMGH (IN REF. 1).
FT			
FT			
SQ	SEQUENCE	507 AA; 56469 MW; 85721c6E024575EF CRC64;	
	Query Match	9.5%; Score 337.5; DB 1; Length 507;	
	Best Local Similarity	32.6%; Pred. No. 7.2e-13;	
	Matches	90; Conservative 47; Mismatches 10; Indels 49; Gaps 11	
OY		21 AELDGGGKSLCCHRTQGLMI-MKYTYKKGPCNLEHNEALLFEAKMMNRRLRHSRVALL 79	
Dd		239 AQIGEGGEAV-----LQGYLYGQKVAVKIKCVTAQAFLDELTAVMTKMQHMLIVRL 292	
OY		80 GVILEEGKYSLVMEEMEKGNIMHYAKAEMSTPLSVKGRLL-----LELEGMCYL 129	
Dd		293 GVILLHGILY-LVMEIVSKGNLVNPLR-----TRGALVNVTLOALFSLHVAEGMEYL 343	
OY		130 HGKGVIHKDLKPENILVDNDPHIRIADLGIAFSFKMSKLNNBEHNELREVDGTAKNGGT 189	
Dd		344 ESKRLVHRDDLARNILVISEDVLAVKSDPEGLAK-----AERKGLDSRL----P 387	
OY		190 LYYAAPHELNVANKPTEKSDVYSFAVVLAIFA-NKEPTYENAICEOOLINCISGNPD 248	
Dd		388 VKWPAPEALK-HGKFTISKDVWSFGVLIWEVFSGRAYPER-MSLKREVSAAVEKGYRME 444	
OY		249 VDDITECPREIIISLMKLCWFANSEARPTEPGIEEK 284	
Dd		445 P---PPEGDPGVHVLMSSCWAEAPARRRPFEEKLEK 477	

Search completed: June 21, 2003, 16:13:13
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2003, 16:05:19 ; Search time 87 Seconds
(Without alignments)
1589.168 Million cell updates/sec

Title: US-09-981-397a-16
Perfect score: 3545
Sequence: 1 MOPDMSLVNFKKMSDFLES.....ALHOCGRIDLSSLIYVSON 671

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp._archaea:*
2: sp._bacteria:*
3: sp._fungi:*
4: sp._human:*
5: sp._invertebrate:*
6: sp._mammal:*
7: sp._mhc:*
8: sp._organelle:*
9: sp._plant:*
10: sp._rodent:*
11: sp._virus:*
12: sp._vertebrate:*
13: sp._unclassified:*
14: sp._virus:*
15: sp._bacteriaph:*
16: sp._archaeap:*
17: sp._archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	410.5	11.6	786	11 Q9ERK0	Q9ERK0 mus musculi
2	387	10.9	784	4 Q96T11	Q96T11 homo sapien
3	384	10.8	784	4 Q9H4D1	Q9H4D1 homo sapien
4	384	10.8	784	4 Q96KH0	Q96KH0 homo sapien
5	361.5	10.2	1412	13 Q80W84	Q80W84 paraliichthy
6	360.5	10.2	669	13 Q91AA2	Q91AA2 paraliichthy
7	348	9.8	609	13 Q91776	Q91776 xenopus lae
8	347.5	9.8	1671	5 Q9N1V5	Q9N1V5 xenopus lae
9	346.5	9.8	1418	13 Q80W83	Q80W83 paraliichthy
10	345.5	9.7	515	13 Q80UY9	Q80UY9 brachydanio
11	340.5	9.6	855	5 Q01700	Q01700 caenorhabdi
12	339	9.6	488	13 Q13064	Q13064 xenopus lae
13	339	9.6	1358	13 Q73798	Q73798 xenopus lae
14	338.5	9.5	465	11 Q9D6H7	Q9D6H7 mus musculi
15	338.5	9.5	465	11 P70223	P70223 mus musculi
16	338.5	9.5	511	11 Q64103	Q64103 mus sp. vnk

17	338.5	9.5	763	10 Q9C903	Q9C903 arabidopsis
18	338.5	9.5	1245	13 Q9YGH8	Q9YGH8 scophthalmu
19	338	9.5	1371	11 Q90YWA	Q90YWA rattus sp.
20	337.5	9.5	523	4 Q9NSR8	Q9NSR8 homo sapien
21	337.5	9.5	777	10 Q9C833	Q9C833 arabidopsis
22	337	9.5	989	13 Q9PWN6	Q9PWN6 gallus gall
23	336.5	9.5	1171	10 Q9STG4	Q9STG4 arabidopsis
24	335	9.4	525	10 Q8W022	Q8W022 arabidopsis
25	335	9.4	829	10 Q24027	Q24027 lycopersico
26	334.5	9.4	1094	5 Q23915	Q23915 dictyostell
27	334	9.4	765	10 Q93YU0	Q93YU0 arabidopsis
28	334	9.4	1127	5 Q908P5	Q908P5 diadema set
29	331	9.3	525	10 Q9F1L6	Q9F1L6 arabidopsis
30	331	9.3	806	10 Q9ZSD8	Q9ZSD8 lycopersico
31	331	9.3	829	10 Q9ZSD9	Q9ZSD9 lycopersico
32	330.5	9.3	527	5 Q9B125	Q9B125 dictyostell
33	330.5	9.3	1418	13 Q93457	Q93457 scophthalmu
34	329.5	9.3	475	10 Q9STG5	Q9STG5 arabidopsis
35	329.5	9.3	2144	5 Q9VD94	Q9VD94 drosophila
36	329	9.3	502	13 Q9DDK6	Q9DDK6 salmo salar
37	329	9.3	1257	10 Q64768	Q64768 arabidopsis
38	329	9.3	1362	13 Q9PVZ4	Q9PVZ4 xenopus lae
39	329	9.3	1368	13 Q80W85	Q80W85 paraliichthy
40	328.5	9.3	405	10 Q9LVQ9	Q9LVQ9 arabidopsis
41	328.5	9.3	450	11 Q8VCW1	Q8VCW1 mus musculi
42	328.5	9.3	480	10 Q9FVQ7	Q9FVQ7 faqus sylva
43	328.5	9.3	773	10 Q9C902	Q9C902 arabidopsis
44	328.5	9.3	1369	13 Q80W86	Q80W86 paraliichthy
45	328	9.3	465	4 Q16176	Q16176 homo sapien

ALIGNMENTS

RESULT 1
ID Q9ERK0 PRELIMINARY: PRT: 786 AA.
AC Q9ERK0:
DT 01-MAR-2001 (TREMUREL 16, Created)
DT 01-MAR-2002 (TREMUREL 20, Last sequence update)
DT 01-JUN-2002 (TREMUREL 21, Last annotation update)
DE PKC-regulated kinase PKK.
GN ANKRD3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPTRAIN=BALB/C;
RA Chen L., Haidar K., Cariappa A., Pillai S.;
RX MEDLINE=21293027; Pubmed=11278382;
RA Chen L., Haidar K., Ponda M., Cariappa A., Rowitch D., Pillai S.;
RT "Protein kinase C-associated kinase (PKK), a novel membrane-associated, ankyrin repeat-containing protein kinase."
RT associated, ankyrin repeat-containing protein kinase."
RN [2]
J1 J. Biol. Chem. 276:21737-21744(2001).
RP SEQUENCE FROM N.A.
RC SPTRAIN=BALB/C;
RA Chen L., Haidar K., Cariappa A., Pillai S.;
RX Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF302127; AGC30871.2; -
DR HSSP: P25963; I1KN.
DR MGD: MGI:1919638; Ankrd3.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF000023; ank. 10.
DR Pfam: PF000069; pkinase. 1.
DR PRINTS: PR01415; ANKYRIN.
DR PRODOM: PD0000001; Euk_pkinase. 1.
DR SMART: SM00248; ANK. 10.
DR SMART: SM00220; S_TKc. 1.


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DR InterPro: IPR002011; RTKInaseII.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00757; Furin-like; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF01030; Recep_L_domaln; 2.
DR PRINTS: PR00014; ENTPEI1.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk_pkinase; 1.
DR SMART: SM00060; FN3; 3.
DR SMART: SM00261; FU; 1.
DR SMART: SM00220; S_tkc; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; UNKNOWN_1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 1412 AA; 158944 MW; 140759FB633A3A9 CRC64;

Query Match 10.2%; Score 361.5; DB 13; Length 1412;
Best Local Similarity 28.2%; Pred. No. 1.6e-15;
Matches 125; Conservative 64; Mismatches 156; Indels 99; Gaps 19;

DR 22 ELDSGGEGKVSLOCFHRTQGL-----MIMKTVKGPNCIEHNEALLEAKMMNR 69
DB 1003 ELDSGGEGGV-----YEGLAGGVAKDEPETRVAIKTVNESASMRERIE-FLNEASVMKE 1055

QY 70 LRHSRYVKLLGVIIIEGKYSLVMEYMEKGL--MHVLAEMST-----PLSVKGRILLIE 121
DB 1056 FNCHHVVRLGVVSGQPTLVIMELMTRGDLKSHLSLRKRENTTQVLPLKMIQWAGE 1115

QY 122 IIEGKCYLHGKGVIIHDKPENILVNDPFHRIADGLASFKMSKLNNEHNELEVDG 181
DB 1116 IAGMAYVLANKKRVHNDLARNQMAEDFAVKIGDGMT-----RDIYETDY 1162

QY 182 TAKKNGTLL--YMAPEHLNDVNAKPTESDYSFAVVIWAIFA-NKEPYENALCEQOLI 238
DB 1163 YRGGGGLLPVRMWSPESLKD--GVFTTMSDVMSFGVLMETATLAEOFYQGSNBOVLN 1220

QY 239 MCJKSG--NRPDVDITCYCPREIISLMKLCWFANPEARPTFGIEKFRPFYLSQLES 296
DB 1221 FVMEGGGLDKPD-----NCPDMLFELMRWCQYNKMRPSFLEI-----ISSIKKE 1266

QY 297 VERDVSLKKEYSNEN-----AVYKRMQSLQD-----CVAVPSRSNSGATQ 339
DB 1267 LSPFPEMSPFYSEENKPPDTEELDMVENMENIPLDPASTROPASVAAPSSCGTGTTP 1326

QY 340 PGLSHSSQGLG-----MGVYESWFAF--SLEHPQE-----ENEP--SIQSKLD 379
DB 1327 PSNQQLSPMQGPSTPLGVPSPSSGPVASALASPGQALDKHSGHANGPVVLLRPND 1386

QY 380 DEANY-HLYGRMDROTQKOPRON 402
DB 1387 EMOPYAHMNGRKNERALLPQSS 1410

RESULT 6
Q91AA2 PRELIMINARY; PRT; 669 AA.
AC Q91AA2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Insulin-like growth factor 1 receptor 1 (Fragment).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_Taxid=7957;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC TISSUE=RETINA;
RA Otteson D.C., Cirenza P.F., Hitchcock P.F.;
RT "Molecular cloning and expression of igf-1 and igf-1 receptor in the
RT normal and regenerating retinas of goldfish."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: AF216772; AAF63263.1; -.
DR HSSP: P06213; 11RK.
DR InterPro: IPR007719; Euk_pkinase.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR002011; RTKInaseII.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk_pkinase; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
KW Glycoprotein; Phosphorylation; Receptor; Transmembrane;
KW Tyrosine-protein kinase.
FT NON TER 1
SQ SEQUENCE 669 AA; 75047 MW; 41EBB879A371000 CRC64;

Query Match 10.2%; Score 360.5; DB 13; Length 669;
Best Local Similarity 27.5%; Pred. No. 6.3e-16;
Matches 120; Conservative 60; Mismatches 154; Indels 103; Gaps 16;

QY 22 ELDSGGEGGV-----SLOCFHRTQGLMIMKTVKGGKNCIEHNEALLEAKMMNR 75
DB 278 ELDSGGEGGVYBSIANGGVAKDEPETRVAIKTVNESASLHERIE-FLNEASVMKEFNCHV 336

QY 76 VKLLGVIIIEGKYSLVMEYMEKGLMHVLAEMST-----PLSVKGRILLIEEGM 126
DB 337 VRLGVVSGQPTLVIMELMTRGDLKSHLSRSASNTSSLPPLKMIQWAGETADQM 396

QY 127 CYLHGKGVIIHDKPENILVNDPFHRIADGLASFKMSKLNNEHNELEVDGTAKKN 186
DB 397 AYHLAKFVRHDLARNQMAEDFTVKIGDFGT-----RDIYETDYRKGG 443

QY 187 GGTLL--YMAPEHLNDVNAKPTESDYSFAVVIWAIFA-NKEPYENALCEQOLIMCIS 243
DB 444 KGLLPVRMWSPESLKD--GVFTTMSDVMSFGVLMETATLAEOFYQGSNEOVLRFVMEG 501

QY 244 G--NRPDVDITCYCPREIISLMKLCWFANPEARPTFGIEKFRPFYLSQLESVEEDY 301
DB 502 GILDKRD-----NCDMLFELMRWCQYNKMRPSFLEI-----ISSIKDLEAGF 547

QY 302 KSLIKKEYSNENAVYKRMQSLQDCVAVPSSRSNSATQPGSLHSSQGLMGVYESWFAF 361
DB 548 KEMSPFYSEEN--KEPDTEELDMENV-GAMENVLPLEPSSLP-----LAP 590

QY 362 SLEHPQE-----ENEPS--IQSKIDDEANY-H 385
DB 591 SLASPGQCAPASOGSSSPAGSSPPPPAPRTSTNSPASANGPSVVLASFDEQOPYAH 650

QY 386 IYGRMDROTQKOPRON 402
DB 651 MNGGRKNERALLPQSS 667

RESULT 7
Q91776 PRELIMINARY; PRT; 609 AA.
AC Q91776;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
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AC	09NVT5:	DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)		
DE	Insulin-related peptide receptor.		
OS	Biomphalaria glabrata (Bloodfuke planorbh).		
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;		
OC	Planorbidae; Biomphalaria.		
OX	NCBI_TaxID=6526;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Lardans V., Coplin J.-F., Dissous C.;		
RT	"Characterization of a Biomphalaria glabrata insulin-related peptide		
RT	receptor."		
RL	Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.		
CC	-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN		
CC	TYROSINE PHOSPHATE.		
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).		
DR	EMBL; AF1011195; AACF1166.1; .		
DR	HSSP; P06213; IIRK.		
DR	InterPro; IPR000494; EGFR_L_domain.		
DR	InterPro; IPR000719; Euk_kinase.		
DR	InterPro; IPR003961; FN_III.		
DR	InterPro; IPR002174; Furin-like.		
DR	InterPro; IPR002011; RTK_inse1t.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	InterPro; IPR002221; MAP.		
DR	Pfam; PF00041; fn3; 2.		
DR	Pfam; PF00757; Furin-like; 1.		
DR	Pfam; PF00069; kinase; 1.		
DR	Pfam; PF01030; Recep_L_domain; 2.		
DR	PRINTS; PRK0109; TYRKINASE.		
DR	ProDom; PD000001; Euk_kinase; 1.		
DR	SMART; SM00060; FN3; 2.		
DR	SMART; SM00261; FU; 1.		
DR	SMART; SM00219; TYRKC; 1.		
DR	PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN; 1.		
DR	PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		
DR	PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.		
KW	ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;		
KW	Transmembrane; Tyrosine-protein kinase.		
SQ	SEQUENCE 1671 AA; 18838 MW; D3947C8109A553E3 CRC64;		
Query Match	9.8%; Score 347.5; DA 5; Length 1671;		
Best Local Similarity	22.3%; Pred. No. 1.8e-14;		
Matches 147;	Conservative 107; Mismatches 264; Indels 141; Gaps 26;		
QY	22 ELDSGSGFGKSLYLCNHTQGL-----MIKTVYKGNPCIEHNALLEAKKM 67		
DB	1032 ELGGSGSGMW-----YEGIAKGLRDDDEEELIYVAVKTVNERANFTDQCE-FLNENTIM 1084		
QY	68 NLRHRSRVKLLGVITIEBKYSIVMEYMEKGNL--MHVIAKEMSTPLSVKGRILL-- 120		
DB	1085 KAFCHGHVHVGLGVASRANRYVVMELMRDGLDTLYLOQLRPDEHFPATPTLEILLM 1144		
QY	121 --ELIEEGSCYLHGSGVNIHKDKLRNNILVNDNFHIKIDLGASRKMSKLNNEHNELRE 178		
DB	1145 TGEIADGNAVYADDKFVHRDIAARNCMVAGRTYKVGDFGMT-----RDVYE 1191		
QY	179 VDTAKKNGGTL--YUVAPEHLNDVNAKPTKSDVYSFAVLM-AIFANKPEYNAICEQ 235		
DB	1192 TDYRKRGKGKMLPRVMAAPESLKD--GVFSSMSQCSWSGVYLMEVTLAOPYO-GLSNE 1248		
QY	236 QLMICIKSGNRPVDITTEYCSPREIISLMKLCWEANDEAPRTFGIEKRPFLYSOLEE 295		
DB	1249 EVVFFVVDGH--VMDIPENDCEEMAFMLRCLWEERRRKPRTFFKAVIK---FLLPKLS 1301		
QY	296 SVEEDVASTIKKEVSNEN-----AVVKMQSLQDDCAVPSRSNSA 336		
DB	1302 SFEEV---VSFFYSSGSDTHDAGAPGNILEFEGTLEILIEREDATINSFICEGAAAPKQ 1357		

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QY 337 TEOPGSLHSSQGLMGVPEESWFPASLE-----HQEENPESLSQKLQDEANYHLHYGS 389
D 1358 SLLPQS--NAEGNSQFGITETVFOQDDELVLPGYQNDNDEDCFISFGDDVDSSQPF 1415
QY 390 RMDQOTQ-QPQWAVANREERERRRYS--HDPPAQORPYENFQNTG-----KQTVSSA 442
D 1416 MPESHSTSSVNRQPLSHQSHHNSGSEASLHNSGLIEKKPLTKKRSRQSPSKOTIIPRP 1475
QY 443 ASHGNAVHOPSGLSQPOVLVYQNNGLYSSHGFTGRPLDPTAGPR--WVYPIPSHMPSL 500
D 1476 VEYLD--HGPEPLMKPD---PRSSLQNNPFSTSTADPLRLGPHNTIASSNLPGLVSR 1530
QY 501 HNIVPEPTNIGNTPTMPFSSL-----PPTDESI-----529
D 1531 PNLRLP---VLSPPPTGFKFIVSOHNSGDMTDAGRODKPPSGQPIVTHPAPLANLVHE 1587
QY 530 -KYIYSTGTGLOIAVYVMEIGTSSSLDSTNTNFKEEPAKKQAFIDNTTSLTDHL 587
D 1588 NELESPQATGSLSDQHT-----SSTPAIATNTSSDGSKESTKSESFSLRNGLTNGHI 1642

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RESULT 9

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ID 08UW83 PRELIMINARY: PRT: 1418 AA.
AC 08UW83;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Type 1 Insulin-like growth factor receptor.
GN FIGF-IR-2.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
OC NCBI_Taxid=8255;
RN 11
RP SEQUENCE FROM N.A.
RA Nakaio N., Tanaka M., Higashimoto Y., Nakashima K.;
RT "Identification and characterization of four distinct subtypes of
RT insulin and type 1 insulin-like growth factor receptors in flounder,
RT Paralicthys olivaceus.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB065099; BAB83670.1;
DR InterPro: IPR000494; EGFR_L_domain.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR002011; RTkinaseII.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00757; Furin-like; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00060; FN3; 3.
DR SMART: SM00261; FU; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_ITI; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1418 AA; 159651 MW; 0BA6174D2E3B2D34 CRC64;

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Query Match 9.8%; Score 346.5; DB 13; Length 1418;
 Best Local Similarity 28.5%; Pred. No. 1.6e-14;
 Matches 119; Conservative 60; Mismatches 148; Indels 91; Gaps 18;

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QY 20 SAELDSGFGKVSLSCHFRTQGL-----MIKTVYKGNPCIEHNEALIEPAKM 67
D 1005 SRELQGSFGNV-----YESLANGVYKDEPETRVAIKTVNESASMERIE-FLNEASVM 1057
QY 68 NLRHSHVYKLLGVILIEGKSLVMEYKGNLHVLR-----AENSTP-----LS 113
D 1058 KEFNCNHVYRLIGVSGQPTLIVIMELMTGDKLSYLRPKRQQWSLILPLKMLQ 1117
QY 114 VKGRILIEIEGKYLHGKGVYIHKDLKPENLVNDNPHITADIGLASPFMWSKLNNEH 173
D 1118 MAG-----QIADGMAYLVANRKFVHRDLAARCMVAEDIVYKIGDFGWT-----1160
QY 174 NELREVDGTAKKNGTL--YVMAPEHLVDVNAKPTKSDYVSAVYVLAIFA-NKEPYEN 230
D 1161 RDIYETDYRRKGGGLLPVRMWSPESLKD--GVFTTSDVWSGCVYVIMELSTLAEOPYG 1218
QY 231 AICQQLIMCIKSG--NRPDVDTTEYCPREIISLKLCEANDPEARPTFGIEKFRPF 288
D 1219 LSNQVLRFWVEGGLLEKRP-----QNCPLMELFMRMCWQYNPKMRPSFVEI-----1265
QY 289 YLSQLESVEDEVKSLKEYSENNAVYKRNQSLQDQV-----AVPSRSMSATDQPSLH 344
D 1266 -ISLKLDELSVEFSEVSEFFYSADKPSSE-QQVHLQKMDNIEDVPADQPSST--QPOQAQ 1321
QY 345 SSQGLGMGPVEESWFPASLEHPOEENPESLSQKLQDEANYHLGSRMDRQTKQOPRON 402
D 1322 VPQGTTPSPSEAPAPASIS-PSSPSSPCST-----AAMDKQASQQAAN 1366

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RESULT 10

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ID 08UUY9 PRELIMINARY: PRT: 515 AA.
AC 08UUY9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Insulin-like growth factor I receptor (Fragment).
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_Taxid=7955;
RN 11
RP SEQUENCE FROM N.A.
RA Cheng R., Wu J.-L.;
RT "Cloning and embryonic expression of zebrafish (Danio rerio) insulin-
RT like growth factor-I receptor and its relationship with p53 tumor
RT suppressor gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY043191; AAL05594.1; -.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002011; RTkinaseII.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_ITI; UNKNOWN_1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 515 AA; 57342 MW; CC28FC34AA0242D3 CRC64;

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Query Match 9.7%; Score 345.5; DB 13; Length 515;
 Best Local Similarity 27.8%; Pred. No. 4.4e-15;
 Matches 121; Conservative 56; Mismatches 160; Indels 99; Gaps 16;


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OY 22 ELDSGSGFKV-----SLCFHRTQIGIMIKTYKKGPNCEIHNHALLLEEKMMNRLSRSV 75
   || || || || || || || || || || || || || || || || || || || || ||
Db 127 ELGSGSFGCMVYEGIAKGVKDEPFRVAIKTYNESLSHERIE-FLINEASVMKEFNCNV 185
   || || || || || || || || || || || || || || || || || || || || ||
OY 76 VKLLGVITIECKYSLVMEYMEKGNIMHVLKAEKST-----PLSVGRILLIETIEGM 126
   || || || || || || || || || || || || || || || || || || || || ||
Db 186 VRLLEVSOGOPTLVIMEIMLTGDLKSYLRSLRSVENTSSLPLRPKKMIQMAGEIADGM 245
   || || || || || || || || || || || || || || || || || || || || ||
OY 127 CYLHGKGVINHDLRKENIIVYNDPFHKTADLDGLASKMKMSKLNNEHNELREVDGTAKKN 186
   || || || || || || || || || || || || || || || || || || || || ||
Db 246 AYLNANKFVHRDLAARNCVADPELYVKIGDFGKT-----RDLYEDYRYRKG 292
   || || || || || || || || || || || || || || || || || || || || ||
OY 187 GGTI--YYMADEHLNDVNAKPYEKSVDYSFVAVLMAIFA-NKPEYENALCEOOLIMCIS 243
   || || || || || || || || || || || || || || || || || || || || ||
Db 293 KGLLPVRMMSPESLND--GVFTTMSDVSMEFGVYIMLIALADEPYGMSMEGYLRRVMEG 350
   || || || || || || || || || || || || || || || || || || || || ||
OY 244 G--NRPDVDDITIECPRELISLMKLCWEANPEARPPGIEKEKFRFYLSOLEESVEDY 301
   || || || || || || || || || || || || || || || || || || || || ||
Db 351 GULDPD-----NCPDMLEFMRMCWOYNPKRKPSFLBI-----ISSIEDLEAGF 386
   || || || || || || || || || || || || || || || || || || || || ||
OY 302 KSIAKREYENENAVVRMOSLOLDCYAVPSSRSNSATDEQSGLSHSSOGLGMPVEESWAP 361
   || || || || || || || || || || || || || || || || || || || || ||
Db 397 KETSFYEEEN--KPPDEEELDMENV-GTMEENVLPLEBSSSLP-----LAP 439
   || || || || || || || || || || || || || || || || || || || || ||
OY 362 SLEHPOE-----ENEPSSLOSLDDEANHYHLGSRMDROTROOPRONVAYNREEE 410
   || || || || || || || || || || || || || || || || || || || || ||
Db 440 SISPPQOCTAAASCCSSPSSPPSSPS-----STDKHPLPTSAANGPS- 481
   || || || || || || || || || || || || || || || || || || || || ||
OY 411 RRRRYSHPFAOQRPY 426
   || || || || || || || || || || || || || || || || || || || || ||
Db 482 ---MYLRGPFEEGOPY 494
   || || || || || || || || || || || || || || || || || || || || ||

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ID	001700	PRELIMINARY;	PRT;	855 AA.
AC	001700;			
DT	01-JUL-1997 (TrEMBLrel. 04, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-MAY-2002 (TrEMBLrel. 20, Last annotation update)			
DE	Hypothetical 95.1 kDa protein F33E2.2.			
GN	F33E2.2.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Lennard N.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
CC	!- SIMILARITY: BELONGS TO THE EMBL/GenBank/DBJ databases.			
DR	EMBL; AL022593; CAI18635.2; -.			
DR	EMBL; Z84574; CAI18635.2; JOINED.			
DR	EMBL; Z84574; CAB06544.2; -.			
DR	EMBL; AL022593; CAB06544.2; JOINED.			
DR	InterPro: IPR000719; Euk. kinase.			
DR	InterPro: IPR002290; Ser. thr. kinase.			
DR	InterPro: IPR004040; STY. kinase.			
DR	InterPro: IPR001245; TYL. kinase.			
DR	Plam; PF00069; pkinase; 1.			
DR	PRINTS; PR00109; TYRKINASE.			
DR	ProDom; PD000001; Euk. kinase; 1.			
DR	SMART; SMO0221; STYKc; 1.			
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Hypothetical protein; Serine/threonine-protein kinase; Transferase.			
SQ	SEQUENCE 855 AA; 95786 MW; F44DD2538CB7D95A CRC64;			

Query Match	9.68;	Score 340.5;	DB 5;	Length 855;
Best Local Similarity	22.98;	Pred. No. 2e-14;		
Matches 162;	Conservative 94;	Mismatches 259;	Indels 191;	Gaps 28

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0Y 13 KSSD-----ELESADGSGFGXKSLCFHROGIMIKTYKPKNCJENHEALLE-EAK 65
Db 49 KSDEIEMELDPDAISLEWLGSSGCAV--RGOLENRV--ARKVNOJKEFEIK 1000
0Y 66 MMRRLHRSRVKLLGYLIEEGYSLVMEJMEKGNLMHLYKAEKSTPLSVGRILLETIEG 1250
Db 101 HLMHRIKHOINTELFGXCSKSPCYLMEKCSGOLCTYLSKRNRITITRELFQWVKELADG 1600
0Y 126 MCLHGKGYLHKDKPENTLVNDNFIKADLGASFKMMSKLNNEEHELREVDGTAKK 1850
Db 161 MHYLNQKVIHNRDKSPNLLISAEDSIKIDEGTSHM-----KKMDSTWMS 2070
0Y 186 NGGLTYMAREHLDVNAKP-TEKSDYSFAVVLMAITANKERPEMAICEDOLIMCKSG 2440
Db 208 FCGTYSMMAREM--TKROPCNEKVDVYSFGVVLMEMLTRETPLYAN-IAQMAITFGVTN 2630
0Y 245 --NRPVDDITCECREEITSLMKLOEANPEARPFRCIE--EKPRFPLYSOLEE---- 2950
Db 264 ILSLP--MPEARGLVLLIKOLLSQKGRNRPSFSHROHMEIFKPELFEMTEEBWOL 3190
0Y 296 -----SVEEDVKSLEKYESENNAVVKMOSLDVCV 3260
Db 320 AMDSYREPAKCIQYESTVTRHDGCRKSAFAMEEELQKRHNHOLDIRMYEMKL--- 3760
0Y 327 AVPSRSNSATQEDPGSLHSSGCLGMRYEESWFAELENHOEENRPSLOSKLODEANYHL 3860
Db 377 ----KRTNMKYDLOQCFTELKLESELA-EWEKDLTEREOMHONQNSPKAAVAPRAOLRG 4310
0Y 387 YGSR----MDROKQOORONAVUN-REERRRRVRVSHDFQAQORYENFOUNTEGCTYSS 4410
Db 432 YPNEGVDMDSSDEVDYPCRGSPYKCSNNTSSSGVQSSFRQ-----SSRSASGOOTRSE 4480
0Y 442 AA-----SHGNANVHOPSGLTS----- 4570
Db 489 GANPKRLRNDALIRHSGSYWETLGGARGPSPADDSFSDSGMSMAGACSTAITNGSGOY 5480
0Y 458 -QPOVLXON-NGLYSHSGFTR----PLDPQTA--GRVWY-RPIDSMBLSHNT---P 5040
Db 549 CYSQTLIYRNODGRWSDGRIASRRRVSTVSNKSTAVPQGVFFGRDPSRVP--HGVISCS 6060
0Y 505 VPETNLTGNTPTWPESSLP-----PRIDESIKTTIYNSTGIGIAGIANYEIG 5500
Db 607 SPSSSKLNKNSVSPSRNAPHOLEDGCCAHARAPAKSIAPVM----- 6490
0Y 551 GTSSSLDSTNTNFKKEPRAKQALFEDNTTSLTKOHDPRENLGK 596
Db 650 -TSS-----RARSPTPYDNDPEWAKESVDESPKLNKLEK 685

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RESULT 12	ID	013064	PRELIMINARY;	PRT;	488 AA.
AC	013064;				
DT	01-JUL-1997 (TREMBLrel. 04, Created)				
DT	01-JUL-1997 (TREMBLrel. 04, last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, last annotation update)				
DE	Lyn protein tyrosine kinase..				
GN	LYN.				
OS	Xenopus laevis (African clawed frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;				
OC	Xenopodidae; Xenopus.				
OX	NCBI_TaxID=8355;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Fukami Y., Funabiki K., Sato K.;				
RT	"Nucleotide sequence of Xenopus Lyn protein tyrosine kinase."				
RL	Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.				
CC	-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.				
DR	EMBL: AB003358; BAA20078.1; -				
DR	HSSP: P08631; IAD5				
DR	InterPro: IPR000719; Euk_pkinase.				
DR	InterPro: IPR000980; SH2.				

Query Match	9.6%	Score 339,	DB 13,	Length 488,
Best Local Similarity	33.1%	Pred No. 1.1e-14,		
Matches	92,	Conservative	49,	Mismatches 99,
				Indels 38,
				Gaps 11.

RESULT 13
073798
ID 073798 PRELIMINARY; PRT; 1358 AA

Query Match	Best Local Similarity	Score	DB	Length
Matches	Conservative	62	Mismatches	146
			Indels	94
			Gaps	18
DR InterPro: IPR000494; EGFR_L domain.				
DR InterPro: IPR0000719; Euk_pkinase.				
DR InterPro: IPR003961; FN_III.				
DR InterPro: IPR002174; Furin-like.				
DR InterPro: IPR002011; RTKaseit.				
DR InterPro: IPR001245; Tyr_pkinase.				
DR Pfam: PF00041; fn3_2.				
DR Pfam: PF00757; Furin-like: 1.				
DR Pfam: PF00659; pkinase: 1.				
DR Pfam: PF01030; Recep_L domain: 2.				
DR PRINTS: PR00109; TYRKINASE.				
DR Prodom: PD000001; Euk_pkinase: 1.				
DR SMART: SM00060; FN3_3.				
DR SMART: SM00261; FU: 1.				
DR SMART: SM00219; TyrcK: 1.				
DR PROSITE: PS00107; PROTEIN_KINASE_ATP: 1.				
DR PROSITE: PS50011; PROTEIN_KINASE_DOM: 1.				
DR PROSITE: PS00109; PROTEIN_KINASE_TYR: 1.				
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_TYR: 1.				
DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Signal;				
KW Transferrase; Glycoprotein; Tyrosine-protein kinase.				
FT SIGNAL	1	25	POTENTIAL	
FT CHAIN	26	734	INSULIN-LIKE GROWTH FACTOR-1 RECEPTOR	
FT FT			ALPHA SUBUNIT.	
FT CHAIN	735	1358	INSULIN-LIKE GROWTH FACTOR-1 RECEPTOR	
FT FT			BETA SUBUNIT.	
SQ SEQUENCE	1358 AA; 153863 MW; 2EA4E1FEA6696776 CRC64;			
Query Match	9.6%	Score 339;	DB 13;	Length 1358;
Best Local Similarity	27.4%;	Pred. No. 4.9e-14;		
Matches	114;	Conservative	62;	Mismatches 146;
				Indels 94;
				Gaps 18;
OY 22 ELDSGEGFEKV-----SLCFHRTQGLIMTKVYKPGKPCIEHNEALLBEAKMMNRLRHSRV 75				
DB 1000 ELGGSGFGMYVEGTAKGVNKNDEATKYAIKYNVNAASMKREIE-FLNEASVMKRFNCHV 1058				
OY 76 VKLLGVITIEBSKYSLWMEYMEKGMIMHYLK-----AESRPLSVKGRITL--ELIE 124				
DB 1059 VRLGVVVSQGGPTVIVIMELMTRGDLKSYLSRLRPDTESNSQGPTR-SLKRMIDWAGEIAD 1117				
OY 125 GMCYTLHGSGVYHKKDKREINLVDDNFHKKIADILASPKMWSKLNNEHNELEKRVGDSTAK 184				
DB 1118 GMSYLNNAKPEFHRDLAARNCVATEDTFYKIGIDEGMT-----KDIYTTDYRK 1164				
OY 185 KNGGTL--YVNAPEHLVDNNAKPTREKSDVYSFAVVLMAITA-NKEPYEMALICEQILMCI 241				
DB 1165 GKGGLLEPVKRWMSPESLKD--GVFTTNSVWMSFGVWLWEIATLAPQAGMSNEQVLETFWM 1222				
OY 242 KSG--NRPDVEDDITVEYCGREILISIMTKIOWNEPAPARPTFPIEKKFRPYILISOLEEVEE 299				
DB 1223 EGGLELEKPD-----NCPMDLFELMRKMCWQNPMPRPSFLET-----ISSIKLDLDP 1268				
OY 300 DVKSILKEKYSNEN-----AAVKRRNSQILDCAVAPSSRSNSATDEPGSLISSQGLG 350				
DB 1269 GKEVSEPFYSSENNKPPOTEELDLDAENNESITPLD-----PSCALONSHHAC--HKS----- 1318				
OY 351 MGPVSESNFAPSLHPDEENEPS--LQSKIQDEANT-HYGSMDRQTYQOQPRON 402				
DB 1319 -----ENGPVVVILRASFDERQPYAHMNGKKNKERALPLDSS 1356				
RESULT 14				
ID Q9D6H7 PRELIMINARY; PRT; 465 AA.				
AC Q9D6H7;				
DT 01-JUN-2001 (Tremblrel, 17, created)				
DT 01-JUN-2001 (Tremblrel, 17, last sequence update)				
DT 01-JUN-2002 (Tremblrel, 21, last annotation update)				
DE Megakaryocyte-associated tyrosine kinase.				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus				

OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa S., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK013606; BAB28926.1; -
 DR HSSP: P11362; 1FGK.
 DR MGD: MGI:99259; Matk.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk.pkinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TYRKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ADP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding; Transferase.
 SQ .SEQUENCE 465 AA; 51615 MW; 8CB0A4CB7CAB9F CRC64;

Query Match 9.5%; Score 338.5; DB 11; Length 465;
 Best Local Similarity 33.6%; Pred. No. 1.1e-14;
 Matches 90; Conservative 46; Mismatches 99; Indels 33; Gaps 10;

21 AELDSGCGFVSLCFHRTGGLMI-MKTIVYKGPICIHNEALLLEAKMMRLRISRYVLL 79
 197 AQLGEGEFQAV-----LQGEYLGQKVAANKIKCDVTAQAFDDETAVMKLQHRNLVRLL 250

80 GVIIIEGKYSLVMEYMEKGNLMHLAKEMSTPLSVKG--RIILEIEGMCYLHGKGVIRK 137
 251 GVILHGLY-IYMEHVSCKGLVNFLETRGRALVYSTQLQFALHVAEGMEYLESKLVHR 309

138 DLKPNILVNDPHFIKIDGLASFKWMSKLNNEEHNELEVDGTAKKNGTLYVYAPPH 197
 310 DLARNILVSEDLVAVSDPGLAK-----AERKGLDSSRL---PVKMTAPEA 353

198 LNDVNAKPTREKSVYSEFAYVLAIFA-NKEPYENALCEOOLLICISGNRPVDDITTEYC 256
 354 LK--NGRFSKSDVSWSEFGLVLEVFYSYGRAPYK-MSLKEVSEAVKGYRMEPPD---GC 407

257 PREIISLMKLCWEANPEARPTPGIEEK 284

Db 408 PGSVHTLMGSCWEANPEARPTPGIEEK 435

RESULT 15
 ID P70223 PRELIMINARY; PRT; 465 AA.
 AC P70223;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE HYL tyrosine kinase.
 GN MATK OR HYLTK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA X C57BL/6; TISSUE=EMBRYONIC STEM;
 RX MEDLINE=96280730; PubMed=8694808;
 RA Hamaguchi I., Yamaguchi N., Suda J., Iwama A., Hirao A., Hashiyama M.,
 RA Aizawa S.I., Suda T.,
 RT "Analysis of CSK homologous kinase (CHK/HYL) in hematopoiesis by
 RT utilizing gene knockout mice."
 RT Biochem. Biophys. Res. Commun. 224:172-179(1996).
 CC -1-SIMILARITY: CONTRAINS 1 SH3 DOMAIN.
 DR EMBL: X83972; CAA58806.1; -
 DR HSSP: P11362; 1FGK.
 DR MGD: MGI:99259; Matk.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR ProDom: PD000001; Euk.pkinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TYRKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ADP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding; kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ .SEQUENCE 465 AA; 51571 MW; 24C2DBA71A08A3B9 CRC64;

Query Match 9.5%; Score 338.5; DB 11; Length 465;
 Best Local Similarity 33.6%; Pred. No. 1.1e-14;
 Matches 90; Conservative 46; Mismatches 99; Indels 33; Gaps 10;

21 AELDSGCGFVSLCFHRTGGLMI-MKTIVYKGPICIHNEALLLEAKMMRLRISRYVLL 79
 197 AQLGEGEFQAV-----LQGEYLGQKVAANKIKCDVTAQAFDDETAVMKLQHRNLVRLL 250

80 GVIIIEGKYSLVMEYMEKGNLMHLAKEMSTPLSVKG--RIILEIEGMCYLHGKGVIRK 137
 251 GVILHGLY-IYMEHVSCKGLVNFLETRGRALVYSTQLQFALHVAEGMEYLESKLVHR 309

138 DLKPNILVNDPHFIKIDGLASFKWMSKLNNEEHNELEVDGTAKKNGTLYVYAPPH 197
 310 DLARNILVSEDLVAVSDPGLAK-----AERKGLDSSRL---PVKMTAPEA 353

198 LNDVNAKPTREKSVYSEFAYVLAIFA-NKEPYENALCEOOLLICISGNRPVDDITTEYC 256
 354 LK--NGRFSKSDVSWSEFGLVLEVFYSYGRAPYK-MSLKEVSEAVKGYRMEPPD---GC 407

257 PREIISLMKLCWEANPEARPTPGIEEK 284

Thu Jun 26 09:21:39 2003

us-09-981-397a-16.rspt

Page 10

Db 408 PGSVHTLMGSCWEAPARRPRKIVEK 435

Search completed: June 21, 2003, 16:14:48
Job time : 90 secs

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Db      1 MOPDMSLVNVIKMKSSDFLESALDSDGFGKVSICFHRTQGLMIMKTVYKGPNCIEHNEAL 60
QY      61 LEEAKMNRRLRHSRYVKLLGVYIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Db      61 LEEAKMNRRLRHSRYVKLLGVYIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
QY      121 EIEEGMCTYHKGKGVTHKDLKRPENILVDNDFHIKIDGLASFKMWSKLNNEEHNELEVD 180
Db      121 EIEEGMCTYHKGKGVTHKDLKRPENILVDNDFHIKIDGLASFKMWSKLNNEEHNELEVD 180
QY      181 GTAKNGGTLYYMAPEHLNDVNAKPTKESDYVSEAVVLMALFANKPEYENALCEQOLIMC 240
Db      181 GTAKNGGTLYYMAPEHLNDVNAKPTKESDYVSEAVVLMALFANKPEYENALCEQOLIMC 240
QY      241 IKSGRNPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKRPFYLSQLEESVEED 300
Db      241 IKSGRNPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKRPFYLSQLEESVEED 300
QY      301 VKSLKKEYSNENAVYKRMQSLQDLCVAVPSSRSNSATBQPSLHSSQGLGMGPVEESWFA 360
Db      301 VKSLKKEYSNENAVYKRMQSLQDLCVAVPSSRSNSATBQPSLHSSQGLGMGPVEESWFA 360
QY      361 PSLEHPOEENPSLQSLQDEANVHLVYGRMDRQTKQOPRONVAVNREERRRRVSHDPF 420
Db      361 PSLEHPOEENPSLQSLQDEANVHLVYGRMDRQTKQOPRONVAVNREERRRRVSHDPF 420
QY      421 AQORRYENFQNTTEGKGTIVYSSAASHGNAVHOPSGLTSPQVLYONNGLYSSHGFGTRPLD 480
Db      421 AQORRYENFQNTTEGKGTIVYSSAASHGNAVHOPSGLTSPQVLYONNGLYSSHGFGTRPLD 480
QY      481 PGTAGPRVWYRPIPSHMPSLNINIVPETNYLGNPTMPFSSLPPTDESIKTYIYNSTGIG 540
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QY      541 IGAYNMEIGTSSSLDSTNTNKEEPAKYOALFNDTTSITDCKHLDPIRENLGKHMKN 600
Db      541 IGAYNMEIGTSSSLDSTNTNKEEPAKYOALFNDTTSITDCKHLDPIRENLGKHMKN 600
QY      601 CARKLGFTQSOIDEIDHDYERDGLKEKYOMLOKVMREGIKGATVGLAQLAHQCSRID 660
Db      601 CARKLGFTQSOIDEIDHDYERDGLKEKYOMLOKVMREGIKGATVGLAQLAHQCSRID 660
QY      661 LLSLIIVYSON 671
Db      661 LLSLIIVYSON 671

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RESULT 2

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US-08-444-005-17
Sequence 17, Application US/08444005
Patent No. 5674734
GENERAL INFORMATION:
APPLICANT: Leder, Phillip
APPLICANT: Seed, Brian
APPLICANT: Stanger, Ben Z.
APPLICANT: Lee, Tae-Ho
APPLICANT: Kim, Emily
TITLE OF INVENTION: CELL DEATH PROTEIN
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,005

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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 00383/026001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-005-17

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Query Match          99.5%; Score 3529; DB 1; Length 709;
Best Local Similarity 99.6%; Pred. No. 1.5e-284;
Matches 668; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db      1 MOPDMSLVNVIKMKSSDFLESALDSDGFGKVSICFHRTQGLMIMKTVYKGPNCIEHNEAL 60
QY      61 LEEAKMNRRLRHSRYVKLLGVYIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Db      61 LEEAKMNRRLRHSRYVKLLGVYIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
QY      121 EIEEGMCTYHKGKGVTHKDLKRPENILVDNDFHIKIDGLASFKMWSKLNNEEHNELEVD 180
Db      121 EIEEGMCTYHKGKGVTHKDLKRPENILVDNDFHIKIDGLASFKMWSKLNNEEHNELEVD 180
QY      181 GTAKNGGTLYYMAPEHLNDVNAKPTKESDYVSEAVVLMALFANKPEYENALCEQOLIMC 240
Db      181 GTAKNGGTLYYMAPEHLNDVNAKPTKESDYVSEAVVLMALFANKPEYENALCEQOLIMC 240
QY      241 IKSGRNPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKRPFYLSQLEESVEED 300
Db      241 IKSGRNPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKRPFYLSQLEESVEED 300
QY      301 VKSLKKEYSNENAVYKRMQSLQDLCVAVPSSRSNSATBQPSLHSSQGLGMGPVEESWFA 360
Db      301 VKSLKKEYSNENAVYKRMQSLQDLCVAVPSSRSNSATBQPSLHSSQGLGMGPVEESWFA 360
QY      361 PSLEHPOEENPSLQSLQDEANVHLVYGRMDRQTKQOPRONVAVNREERRRRVSHDPF 420
Db      361 PSLEHPOEENPSLQSLQDEANVHLVYGRMDRQTKQOPRONVAVNREERRRRVSHDPF 420
QY      421 AQORRYENFQNTTEGKGTIVYSSAASHGNAVHOPSGLTSPQVLYONNGLYSSHGFGTRPLD 480
Db      421 AQORRYENFQNTTEGKGTIVYSSAASHGNAVHOPSGLTSPQVLYONNGLYSSHGFGTRPLD 480
QY      481 PGTAGPRVWYRPIPSHMPSLNINIVPETNYLGNPTMPFSSLPPTDESIKTYIYNSTGIG 540
Db      481 PGTAGPRVWYRPIPSHMPSLNINIVPETNYLGNPTMPFSSLPPTDESIKTYIYNSTGIG 540
QY      541 IGAYNMEIGTSSSLDSTNTNKEEPAKYOALFNDTTSITDCKHLDPIRENLGKHMKN 600
Db      541 IGAYNMEIGTSSSLDSTNTNKEEPAKYOALFNDTTSITDCKHLDPIRENLGKHMKN 600
QY      601 CARKLGFTQSOIDEIDHDYERDGLKEKYOMLOKVMREGIKGATVGLAQLAHQCSRID 660
Db      601 CARKLGFTQSOIDEIDHDYERDGLKEKYOMLOKVMREGIKGATVGLAQLAHQCSRID 660
QY      661 LLSLIIVYSON 671
Db      661 LLSLIIVYSON 671

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RESULT 3

US-08-444-005-15
: Sequence 15, Application US/08444005
: Patent No. 5674734
: GENERAL INFORMATION:
: APPLICANT: Leder, Philip
: APPLICANT: Seed, Brian
: APPLICANT: Stanger, Ben Z.
: APPLICANT: Lee, Tae-Ho
: APPLICANT: Kim, Emily
: TITLE OF INVENTION: CELL DEATH PROTEIN
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street, Suite 3100
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/444,005
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,164
: REFERENCE/DOCKET NUMBER: 00383/026001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 656 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-444-005-15

Query Match 68.4%; Score 2423.5; DB 1; Length 656;
Best Local Similarity 69.8%; Pred. No. 8.4e-193;
Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

QY 1 MOPMSLNVITKMSKSSDPLESAELDSGGFGKYSLCFHRTOGLIMIKTYKGFNCIEHNEAL 60
DB 1 MOPMSLNDITKMASSDLEKTDLDGGFGKYSLCYHSHGFIILKKYTTGPNRAEYEV 60
QY 61 LEEAKMMNRRLHSHSVKLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
DB 61 LEEAKMMNRRLHSHSVKLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
QY 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLASFMMKSLNNEHNEHLEVD 180
DB 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLASFMMKSLNNEHNEHLEVD 180
QY 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLASFMMKSLNNEHNEHLEVD 180
DB 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLASFMMKSLNNEHNEHLEVD 180
QY 181 GTAKK-NGGTLTYAPAPHLNDVNAKPTKPSDVSFAVYVLAIFANKKEPEYENATEOOLIM 239
DB 181 GTAKK-NGGTLTYAPAPHLNDVNAKPTKPSDVSFAVYVLAIFANKKEPEYENATEOOLIM 239
QY 181 GTAKK-NGGTLTYAPAPHLNDVNAKPTKPSDVSFAVYVLAIFANKKEPEYENATEOOLIM 239
DB 181 GTAKK-NGGTLTYAPAPHLNDVNAKPTKPSDVSFAVYVLAIFANKKEPEYENATEOOLIM 239
QY 240 CTKSGNRPDVDDITETCPRETIISLMKLCWEANPEARPTFGIEKFPFYLSOLEEVEE 299
DB 240 CTKSGNRPDVDDITETCPRETIISLMKLCWEANPEARPTFGIEKFPFYLSOLEEVEE 299
QY 241 CTKSGNRPVNEEILEYCPRETIISLMERKQWAIPEDRPTFLGIEEFEPFYLSHPEEYEE 300
DB 241 CTKSGNRPVNEEILEYCPRETIISLMERKQWAIPEDRPTFLGIEEFEPFYLSHPEEYEE 300
QY 300 DVKSLKKEYSNEAVVRMSQLQDCVAVPSRSNSATTEOPGSLHSSQGLGMPVEESWF 359
DB 300 DVKSLKKEYSNEAVVRMSQLQDCVAVPSRSNSATTEOPGSLHSSQGLGMPVEESWF 359
QY 301 DVASLKKEYPDQSPVLRMSFLQHDVCLPLPSPRSNS--EOPGSLHSSQGLGMPVEESWF 358
DB 301 DVASLKKEYPDQSPVLRMSFLQHDVCLPLPSPRSNS--EOPGSLHSSQGLGMPVEESWF 358
QY 360 APSLEHQEENEPISLQKLODEANYHLVYGSMDROTQOQPRQNAVYNNREERRRVSNDP 419

DB 359 SSSPEYQDENDRDRVQAKLOEASVYHAFGICFAEKQTPQPRQNAVYNNREERRRVSNDP 418
QY 420 FAQORPYENFONTECKGTVSSAASHGNVHQPSGLTSQPOVLYQNNGLVSHGFGTRPL 479
DB 419 FAQORPYENFONTECKGTVSSAASHGNVHQPSGLTSQPOVLYQNNGLVSHGFGTRPL 479
QY 480 DPGTAGPRVWYRPIPSHNPISLHNPVPEPTNVLGNTPTMPFESSLPPTDESIXXTYINSGI 539
DB 471 -GTTGCVWYPPNLSQWYSTYKTPVPEPTNPGSTPTMPFSGVADDLKTYTFNSGI 528
QY 540 QIGAVNWEIGTSSSLDSTNTNFKKEPAKYOAITDNTSLFDKHLDPREMIGKHW 599
DB 529 QIGAVNWEIGTSSSLDSTNTNFKKEPAKYOAITDNTSLFDKHLDPREMIGKHW 599
QY 600 NCARKLGFTQSOIDEIDHVERDGLKEKYYOMLQKMWREGIKGATYKLAQALHQCRI 659
DB 585 NCARKLGFTQSOIDEIDHVERDGLKEKYYOMLQKMWREGIKGATYKLAQALHQCRI 644
QY 660 DLLSLTYVSON 671
DB 645 DLLNHLIRASOS 656

RESULT 4
US-09-069-023-28
: Sequence 28, Application US/09069023A
: Patent No. 6348573
: GENERAL INFORMATION:
: APPLICANT: Nunez, Gabriel
: APPLICANT: Inohara, Naohiro
: APPLICANT: Koseki, Takeyoshi
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
: FILE REFERENCE: UM-03333
: CURRENT APPLICATION NUMBER: US/09/069,023A
: CURRENT FILING DATE: 1998-04-27
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO: 28
: LENGTH: 656
: TYPE: PRT
: ORGANISM: Mus musculus
: US-09-069-023-28

Query Match 68.4%; Score 2423.5; DB 4; Length 656;
Best Local Similarity 69.8%; Pred. No. 8.4e-193;
Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

QY 1 MOPMSLNVITKMSKSSDPLESAELDSGGFGKYSLCFHRTOGLIMIKTYKGFNCIEHNEAL 60
DB 1 MOPMSLNDITKMASSDLEKTDLDGGFGKYSLCYHSHGFIILKKYTTGPNRAEYEV 60
QY 61 LEEAKMMNRRLHSHSVKLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
DB 61 LEEAKMMNRRLHSHSVKLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
QY 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLASFMMKSLNNEHNEHLEVD 180
DB 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLASFMMKSLNNEHNEHLEVD 180
QY 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLASFMMKSLNNEHNEHLEVD 180
DB 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLASFMMKSLNNEHNEHLEVD 180
QY 181 GTAKK-NGGTLTYAPAPHLNDVNAKPTKPSDVSFAVYVLAIFANKKEPEYENATEOOLIM 239
DB 181 GTAKK-NGGTLTYAPAPHLNDVNAKPTKPSDVSFAVYVLAIFANKKEPEYENATEOOLIM 239
QY 181 GTAKK-NGGTLTYAPAPHLNDVNAKPTKPSDVSFAVYVLAIFANKKEPEYENATEOOLIM 239
DB 181 GTAKK-NGGTLTYAPAPHLNDVNAKPTKPSDVSFAVYVLAIFANKKEPEYENATEOOLIM 239
QY 240 CTKSGNRPDVDDITETCPRETIISLMKLCWEANPEARPTFGIEKFPFYLSOLEEVEE 299
DB 240 CTKSGNRPDVDDITETCPRETIISLMKLCWEANPEARPTFGIEKFPFYLSOLEEVEE 299
QY 241 CTKSGNRPVNEEILEYCPRETIISLMERKQWAIPEDRPTFLGIEEFEPFYLSHPEEYEE 300
DB 241 CTKSGNRPVNEEILEYCPRETIISLMERKQWAIPEDRPTFLGIEEFEPFYLSHPEEYEE 300
QY 300 DVKSLKKEYSNEAVVRMSQLQDCVAVPSRSNSATTEOPGSLHSSQGLGMPVEESWF 359
DB 301 DVASLKKEYPDQSPVLRMSFLQHDVCLPLPSPRSNS--EOPGSLHSSQGLGMPVEESWF 358


```

Sequence: 5, Application US/09329418
Patient No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ. ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 518
TYPE: PRT
ORGANISM: Dattificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329,418-5

```

Query Match	12.28	Score 433	DB 3	Length 518
Best Local Similarity	25.58	Pred. NO. 1.2e-27		
Matches 146	Conservative 96	Mismatches 184	Indels 146	Gaps 22

```

OY      1L SPSFLSSAEL--DSGGSGKXSLCEFHHTQGLMINKYTKKPCNLEHNEALLPEAKMMNLRH 72
Db      17 STEELNEQELVKGKGGVTFRAOHKRWG-----YDAVRIYVSKALSRVKKMASLDN 69

OY      73 SRVVKLLGYI-----IEEGKYSILVMEYMEKGNLMHVLAKENSTPLSYGRIILEIGMC 127
Db      70 EFLRLREGVIEKMNMDQPKPALYKFKFMEHNSLSLLOSOCPRRPPILCRLLKEVIGMF 129

OY      128 YLHGKG--VIHKDLAPENILVNDHFHKIADLGIALSKFMMSKLNNEEHNEHLEVDGAK- 184
Db      130 YLHDQNPVYLHRDLKPSNVLDPRELHVKLAFGLSTFGGSGQ-----SGTSGS 177

OY      185 KNGGTLYUAPRLNDVNAKPTREKSDVYSFAVALIAEIANKE---PYE-----NAIQEQ 236
Db      178 EPGGTIGYLAPELVFNVNRKASTASDVYSGFLMAAVIAGREVELPEPRLVYEAVCNRQ 237

OY      237 LIMCKISGNRPDVIDTTEYCPRE-----IISLMKLCMEANEPARTF---PGIEEKRFP 287
Db      238 -----NRPSLAELPQAGPEPTPGLEGELKELMQCWSSEPKDRSPFQECPLKIDEVFO- 288

OY      288 FYLSQLEESVEEDYKSLKEKEYSENAVYVKRMOSLOLDCVAVPSSRSNSATEQPSGLHSSQ 347
Db      289 -----WENNNMNAVSVKDFELSQLSSNRRF-----STIPES----- 320

OY      348 GLGGMGVESWFAFSLPHEQENEPSLSLOKLQDEANHYLYLSRMDRQTKQOPRONVAYNR 407
Db      321 --GQGTEMDGCFRRTIENOSHNDVWVSEWL-----NKLNLLEEPSSVKKC 365

OY      408 EE-ERRRRYSHDPFAQGRPEYFNQWTEGKGITYVSSAASHGANVHQPSSLTQSOPLYQNN 466
Db      366 PSLTKRSRAQEEVYQA-----WTAGTSSSMAOP---PQTPETSTFRN 406

OY      467 GLYSHGEGTRPLDPECTAGPRVWYKRPDSHMSPLNINIPETNYLGNTPTWPFSSLDPTD 526
Db      407. QMPS-----PTSTGT-----PS-----PGPRCNOGAEROGMMWCSRRPEP 441

OY      527 ESIK-----YTIYNSGCIQIGAYNMEIGTSS 554
Db      442 NPVTGAPRLVNIYVSGVOYDNNYVLTMOQTAA 473

```

```

RESULT 8
US-09-531-914-3
:
: Sequence 3, Application US/09531914
: Patent No. 6267956
:
: GENERAL INFORMATION:
:
: APPLICANT: ZENECA Limited
:
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
:
: CURRENT APPLICATION NUMBER: US/09/531,914
:
: CURRENT FILING DATE: 2000-03-21

```

```

: PRIOR APPLICATION NUMBER: 09/329,418
:
: PRIOR FILING DATE: 1999-06-11
:
: NUMBER OF SEQ ID NOS: 39
:
: SOFTWARE: FastSeq for Windows Version
: SEQ ID NO 3
:
: LENGTH: 518
:
: TYPE: PRT
:
: ORGANISM: Homo Sapiens
:
: OS-09-531-914-3

```

Query Match	12.28;	Score 433;	DB 4;	Length 518;
Best Local Similarity	25.58;	Pred. NO. 1.2e-27;		
Matches 146;	Conservative 96;	Mismatches 184;	Indels 146;	Gaps 22

QY	1	SSPFLSSAEL--DSGGKGYKSLCFHHPGOLMIKTVYKGRKPCNCEIHNELALBEAKMMNLRH	72
Db	17	STEELENOELVKGKGGVTFRAOHRKWG-----YDAVAVIKVSKALSREVKAMASLDN	69
QY	73	SRVVKLLGVV-----IEEGKYSILMEYMEKGNLHVLAKEKSTPISVYGRITIEIGMC	127
Db	70	EYFLRLEGVIEKYNMQDPKRALYIKRFEMENGLSSLSLOCPKRRPPLICRLKEVIGMF	129
QY	128	YLHGKG--VIHKDLKPENILVDNDFHIKIADLGLASFEMSKLNNEHNELREVDTAK-	184
Db	130	YLHDONDPVLLHRLDKPSNVLLDPELHVKLADGLSTFGSGSQ-----SGTSGG	177
QY	185	KNGGTLYMAPEHLNDVNAKPKTEKSDVYSFAVVLMAITANKE---PYE-----NAITEQ	236
Db	178	EPGGTIGYLAPELVVNNRKASTASDVYSEGLIMAVYLAGREVELPEPISLYEAVCNQ	237
QY	237	LIMCIKSGNRPDDVDITTEYCPRE-----IISLMKLCMEANDEARPTF-----PGIEEKF	287
Db	238	-----NRPSTAEIRPQAGPETPFGLEGELKELMQLCWSSEPKDRSPQECPLPKDEVFQ-	288
QY	288	FVLSOLESEVEDYEDVSKLKEYSENAVYKRMQSLDLCVAVPPSSRSNATEPQCSLHSSQ	347
Db	289	-----WVENNMNAVSIVYKDFLSQLTRSSNRRF-----SLPES-----	320
QY	348	GLGCMGVESWFAPSLHEPQENPESLOSLOKIDEANHYLSRMDRQTKOQPRONAVYNR	407
Db	321	--GOGGTEDMGDFRTTENQHSRNDVYSEWL-----NKLNLLEPPSSVKKC	365
QY	408	EE--ERRRRVSHDPFAOQREYENFQNTGEGKGYSSAASHGNAVHQPSGLTSQPOVLQNN	466
Db	366	PSLTKRSRQOEDVPOQA-----WAGTSSDSMAQP---PQTEPSTIFRN	406
QY	467	GLYSSHGFCGRPLDPGTAGRPVWYRPLDSHMSLNLNIPVETNYLGNTPTWPFSSLPD	526
Db	407	QMS-----PSTGT-----PS-----PGRPGNGQGAERQGNMNSCRPEP	441
QY	527	ESIK-----YTIYNSTGICQIAGVNYEIGTSS	554
Db	442	NPVTGRLVNIYNCSSGVYGDNNYTLMOQDTA	473

US-09/531-914-5
Sequence 5, Application US/09531914
Patent No. 6267956
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/531,914
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 09/329,418
PRIOR FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 518
TYPE: PRT
ORGANISM: DARTFICIAL Sequence

```
; FEATURE:
; OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-5
```

Query Match	12.28;	Score 433;	DB 4;	Length 518;
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Best Local Similarity 25.5%; Pred. No. 1.2e-27;
Matches 146; Conservative 96; Mismatches 184; Indels 146; Gaps 22;

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OY      14  SSDSELSSEL--DSGGFVRSVSLCFHFQOGLMLTKIVYKQPNCEIENHEALLEEAKMNRJPH  72
Db      17  SIELEENELVGKGGFGTVFRAQHRKKMG-----YDAVAVRIVNSKALSREKAAASLDN  69
OY      73  SRVYKLLGVI-----IEBKYSLYMEIWEKGNLHVLAKEMSTPLSVKGRILLEIEBMC  127
Db      70  EFVLLEFVIEKVMNDOPDKPALYVFKFMENGLSGLLSQCPRPAPLLCRLLKEFVLLGMF  129
OY      128  YLHGKG--VIHKDLKPEMLVDNDPHKLTADJGLASFPMKMSKLNNEEHNELREYGVYAK-  184
Db      130  YLHDNDPVLHLRDLKPSNVLLDPELHVLAJDFGLSTFQGGSGO-----SGTSG  177
OY      185  KNGGTLVMAPEHLIDVNAKPTKESDVSFAVLVAIFANKP--PYE-----NAICEQO  236
Db      178  EPGGLGLTGLAPELLFVNVNKRKASTADYVSFGILMAVYLAAGRVELPTEPSLYEAVCNRO  237
OY      237  LIMCIKSGNRDPVDIDITEYCPRE-----IISLKLWEANPEARPTF--PGIEKERP  287
Db      238  -----NPSLAPLPQAGPPTPLFGLJELKELMGQWSESPKDRPSFOCELPKTDVEYQ-  288
OY      288  FYLSQLESSEVEDVAKSLKEYSNEAAVYKRMOSLDLDCAVAVSSKSNKATEDPQSLHSSQ  347
Db      289  -----MVENNMAAAVTVKDFLSQLRSSNRR-----SIPES-----  320
OY      348  GLGMGVPEESWPAFLSEHPOEENERSLOSLOKDDDEANHYLGSRMROTKOCPRONVAVNR  407
Db      321  --GQCGTEMDGFRRTIENOSHNSNDVJWSFWL-----NKLNIIEPPSSVPKKC  365
OY      408  EE-ERRRVRSHDPFAQOORPYENFONTEGKGVTVSSAASHGNAVHOPSGILTSPOVLYONN  466
Db      366  PSLTRKSRQAQEOYVQA-----WTRAGTSSDSMAQP--PQPEHSTFRN  406
OY      467  GLYSHHGFTRLPDGTAGPRVAVYRPIDSHMPSLHNIPYEPETNYIGANTPAPFSLPPND  526
Db      407  QMPS-----PTSTGT-----PS-----PQPRGNOGAEROGNMWSCRTEP  441
OY      527  ESIK-----YTIINSGIOIGAYNMWIEIGTSS  554
Db      442  NPYTGPRPLVNNYNGSGVDVGDNNTYILMQDTTA  473

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OY 14 SSDLEASAEI--DSGGFGVKSLCPRRTGIMTKTVYGGPNCIHEINELLLEAKMMNRLRH 72
Db 17 STEELEQELGKGGFGVTPAQHRKKG-----YDAKTVASKSLSRKVMASADN 69
OY 73 SRVAKLLGVI-----IEGKYSLVMEYMEKGNLMHVLAEMSTPLSVYGRILIEIGMC 127
Db 70 EFVYLRIVSLIEKVMWDDPKRALVTKFKEMNSLSGLGDSQCPRPWPLLCRLKKEVILGMF 129
OY 128 YLHGKG--VIHKDKPENILVNDPFIKIDPLGLASTKRMASKLANNEHNEELREVDTAK- 184
Db 130 YLHQNPNVLLHRDLKPSNVLLDPLHLVYKLAFGSLTGQSGQ-----SGTSG 177
OY 185 KNGGTLVYMADEHNDVNAPKTEKSDVYSFAVYLMAIFANKE---PYE---NAICEQ 236
Db 178 EPGGTGLYLADELVYNNKRASTADVYSFGILMAVYLAGVEVLPTEPILYEAVCNRQ 237
OY 237 LIMCISKGNRPDDVDTIEYCPRE-----IISLMKLCWEANEARTF---PGIEEKRP 287
Db 238 -----NRSLSLELDPQGPETPGLEGKLEMQLCWSSPEKDFQECLEPKTDEVYQ- 288
OY 288 FYLSOLEPSVDEYDKSLKKEYSNENAVYKRMQSLDLCVANPSSRSNATQPOSLSHSQ 347
Db 289 -----MVENNMAAASYVDELSQLRSSNRK-----SIPES----- 320
OY 348 GLGMGPVEESMFAPSLIEHOEENE-----PSL--QSKLDEA 382
Db 321 --GGGCTMDGFRRTIEQHSRNDVMYSEMINKLNLIEPPSSVYKCKCSLKRSAQEQ 378
OY 383 NYHLGSRMDROTKQOPRONVAYNNEEERRRVSHDPAQRPYENFONTEGKTVSSA 442
Db 379 VPOAVTAACTSSDSMAOPQOT-----PETSFRNOMPSTSTGTSPSG----- 420
OY 443 ASHGAAVYQPSGLTSPQPVLYQNGGLYSSHGCTRPDLDPGTAGPRVYWRPIPSHPSLHN 502
Db 421 -PRGQGAERQGMN-----S 435
OY 503 IPVETNLTGLPTMPFSSLPPTDESIKYTYINSTGIGIGAYNMEIGTSS 554
Db 436 CRTPEPNVTGRPLV-----NLYNCGGVGQNNVLTMQGTNA 473

RESULT 11
US-09-531-914-9
; Sequence 9, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531.914
; CURRENT FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-9

```

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; OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-9

Query Match          12.2%; Score 432; DB 3; Length 518;
Best Local Similarity 24.3%; Pred. No. 1.4e-27;
Matches 144; Conservative 91; Mismatches 171; Indels 186; Gaps 20.

```

[illegible]

Db 70 EFVLRLEGVIEKVMDDPKPALVTYKPMENGSLSGLOSQCPRPWPLLCRLKEEVLGMF 129
QY 128 YLHGKG--VIHKDLKPEILVDNDPHIKIADLGLASFPMKSKLNNEEHNELEVDGTA- 184
Db 130 YLHQNPNVLLHRLDKPSNVLLDPELHVKLADFGSLSTOGGSG-----SGTSG 177
QY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVLMATFANKE---PYE-----NAICEQ 236
Db 178 EPGGTGLYLAPELVNVRKASTASDVYSGILMMAYLAGREVELPTEPSLYEAVCNQ 237
QY 237 LIMIKSGNRDVIDITEYCPRE-----IISLMKLCMEANEARPTF---PGIEKFRP 287
Db 238 -----NRSIAELPQAGPETGLGKELMOLCWSSEPKDRPSFOECLPKTDEVFO- 288
QY 288 FYLSOLEESVEDYKSLKKEYSNENAVYKRMQSLQLODCAVPSRSNATQPSLSHSQ 347
Db 289 -----MVENNMAAVSTVKDFLSQLRSSNRF-----STPES----- 320
QY 348 GLGMPVEESWFAFSLLEHPOEENE-----PSL--QSKLODEA 382
Db 321 --GGGTGEMDGFRTIENQHSRNDVVMSEMLKINLEPPSSVPKCKSLTKRSRADOEQ 378
QY 383 NYHLGSRMDROTQOQRONVAYNREERRRRVSHDPAQOQRYENFQTEGKTIVYSSA 442
Db 379 VPOMTAGTSSDSMAQPPQT-----PETSTFRNQMPSTSTGTPSPG----- 420
QY 443 ASHGNAVHQPSGLTSQOVLYQNNGLYSSHGFTRPLDPTGACPRVWYRPIPSHMPSLHN 502
Db 421 -PRNQAEROGMA-----S 435
QY 503 IPVETVYLGNTPTMPFSSLPPTDESIRKTYTINSTGIGIAGVNYMEIGTSS 554
Db 436 CRTEPNPVTGRPLV-----NINCSGVQVGDNNYLTMOQTIA 473

RESULT 12

US-09-329-418-4
Sequence 4, Application US/09329418
Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 518
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-4

Query Match 12.0% Score 425; DB 3; Length 518;
Best Local Similarity 25.3%; Pred. No. 5.4e-27;
Matches 145; Conservative 96; Mismatches 185; Indels 146; Gaps 22;
QY 14 SSDPLESAEL-DSGFGKVSICFHRTOGLMIMKTIVYKGPNCIEHNEALLEEAKMNRRLH 72
Db 17 STELENOELVGKGGFGTVFRAQHRKMG-----YDAVAKTVSKAISREVKAMASLDN 69
QY 73 SRVKKLGLV-----IEGKYSLVMEYMEKGNLMHVLKAENSTPLSVKGRILIEIEGMC 127
Db 70 EFVLRLEGVIEKVMDDPKPALVTYKPMENGSLSGLOSQCPRPWPLLCRLKEEVLGMF 129
QY 128 YLHGKG--VIHKDLKPEILVDNDPHIKIADLGLASFPMKSKLNNEEHNELEVDGTA- 184
Db 130 YLHQNPNVLLHRLDKPSNVLLDPELHVKLADFGSLSTOGGSG-----SGTSG 177
QY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVLMATFANKE---PYE-----NAICEQ 236
Db 178 EPGGTGLYLAPELVNVRKASTASDVYSGILMMAYLAGREVELPTEPSLYEAVCNQ 237
QY 237 LIMIKSGNRDVIDITEYCPRE-----IISLMKLCMEANEARPTF---PGIEKFRP 287
Db 238 -----NRSIAELPQAGPETGLGKELMOLCWSSEPKDRPSFOECLPKTDEVFO- 288

Db 178 EPGGTGLYLAPELVNVRKASTASDVYSGILMMAYLAGREVELPTEPSLYEAVCNQ 237
QY 237 LIMIKSGNRDVIDITEYCPRE-----IISLMKLCMEANEARPTF---PGIEKFRP 287
Db 238 -----NRSIAELPQAGPETGLGKELMOLCWSSEPKDRPSFOECLPKTDEVFO- 288
QY 288 FYLSOLEESVEDYKSLKKEYSNENAVYKRMQSLQLODCAVPSRSNATQPSLSHSQ 347
Db 289 -----MVENNMAAVSTVKDFLSQLRSSNRF-----STPES----- 320
QY 348 GLGMPVEESWFAFSLLEHPOEENEPSLSQLODEANVLYGSRMDROTQOQRONVAYN 407
Db 321 --GGGTGEMDGFRTIENQHSRNDVVMSEMLKINLEPPSSVPKCKSLTKRSRADOEQ 378
QY 408 EE-ERRRVSHPDPAQOQRYENFQTEGKTIVYSSASHGNAVHQPSGLTSQOVLYQN 466
Db 366 PSLTKRSRADOEQVQA-----WTAGTSSDSMAQPPQT-----PQTPETSTFRN 406
QY 467 GLYSSHGFGTRPLDPTGACPRVWYRPIPSHMPSLHNIPVETVYLGNTPTMPFSSLPPTD 526
Db 407 QMPS-----PTSTGT-----PS-----PGRNGAEROGMA-----S 435
QY 527 ESIR---YTYINSTGIGIAGVNYMEIGTSS 554
Db 442 NPVTGRPLVNTINCSGVQVGDNNYLTMOQTIA 473

RESULT 13

US-09-531-914-4
Sequence 4, Application US/09531914
Patent No. 6267956
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/531,914
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 09/329,418
PRIOR FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 518
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-4

Query Match 12.0% Score 425; DB 4; Length 518;
Best Local Similarity 25.3%; Pred. No. 5.4e-27;
Matches 145; Conservative 96; Mismatches 185; Indels 146; Gaps 22;
QY 14 SSDPLESAEL-DSGFGKVSICFHRTOGLMIMKTIVYKGPNCIEHNEALLEEAKMNRRLH 72
Db 17 STELENOELVGKGGFGTVFRAQHRKMG-----YDAVAKTVSKAISREVKAMASLDN 69
QY 73 SRVKKLGLV-----IEGKYSLVMEYMEKGNLMHVLKAENSTPLSVKGRILIEIEGMC 127
Db 70 EFVLRLEGVIEKVMDDPKPALVTYKPMENGSLSGLOSQCPRPWPLLCRLKEEVLGMF 129
QY 128 YLHGKG--VIHKDLKPEILVDNDPHIKIADLGLASFPMKSKLNNEEHNELEVDGTA- 184
Db 130 YLHQNPNVLLHRLDKPSNVLLDPELHVKLADFGSLSTOGGSG-----SGTSG 177
QY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVLMATFANKE---PYE-----NAICEQ 236
Db 178 EPGGTGLYLAPELVNVRKASTASDVYSGILMMAYLAGREVELPTEPSLYEAVCNQ 237
QY 237 LIMIKSGNRDVIDITEYCPRE-----IISLMKLCMEANEARPTF---PGIEKFRP 287
Db 238 -----NRSIAELPQAGPETGLGKELMOLCWSSEPKDRPSFOECLPKTDEVFO- 288

```

QY 288 FYLSQLESVEEDYKSLKKEYSNENAVYKRMOSTLOLDCVAVPSSRSNATBOPSLHSSQ 347
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 -----MVENNMAAAVSTVKDFLSQLRSSNRRF-----SIPES----- 320
QY 348 GLGMPVEESWFAVSLHPOEENESLOSXLQDEANTHLVYSRMDROTQOOPRONAVNR 407
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 321 --GGGTMDGFRRTIENQHSRNDVWVSEWL-----NKLNLPEPSSVRKCC 365
QY 408 EE-ERRRVSHPDPAQORPYENFONTEGKTIVYSSASHGNAHQPSGLTSQPOLVYONN 466
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 366 PSILKRSRAQEEQVPOA-----WTAGTSSDMAOP---PQTPETSPFRN 406
QY 467 GLYSHGCTRPDLPGTAGPRVWRPFPISHNPISLHNITVPETNLGNTPMPFSSLPPTD 526
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 407 QMPS-----PTSTGT-----PS---PGRNGOAGEROGMWSCRPEP 441
QY 527 ESIR-----YTIYNSGICIGAYNYMEIGTSS 554
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 442 NPVTGRPLVNIYINCAGVOYGDNNYITMQTTA 473

```

```

RESULT 14
US-09-329-418-8
; Sequence 8, Application US/09329418
; Patent No. 6096539
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/329,418
; CURRENT FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 420
; SEQ ID NO 8
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Delta Death Domain
US-09-329-418-8

```

```

Query Match 11.7%; Score 414; DB 3; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-26;
Matches 124; Conservative 77; Mismatches 129; Indels 110; Gaps 16;

QY 14 SSDPLESAEL-DSGGFGKVSICFHRTQGLMIMKTYKGPNCIEHNEALLEAKMNRRLH 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 17 STEELNDELVGKGGFGVFRQHRKMG-----YDVAVKIVNSKAISREVKAMASLDN 69
QY 73 SRVVKLLGVITIEG-----KYSLVMEYMEKGNLMHVAKAMSTPLSVKGRITILEIEGM 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 EFLVRLFGVIEKVGSSODPKPALVTKFEMENGLSLGLOSOCPPRPWPLLCRLKEVVLGM 129
QY 127 CYLHGKG--VIHKDLKPNILVNDNFIKIDGLASFKMMSKLNNEHNEHLREVDTAK 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 FYLHDQNPVLLHRDLKPSNVLLDPELHVKLADFGISTFGGSGQ-----SGTGS 177
QY 185 -KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKE---PYE-----NAICEQ 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 GEGGGLGYLAPLEFVNNRKAStADSVYSGILMAYVLAGEVELPTEPSLYEAVCNR 237
QY 236 OLIMCKSGNRPDVIDITEYCPRE-----IISLKLCEANPEARPTF---PGLIEKFR 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 Q-----NPSLAELPQAGPETPGLGLEKELMQLCWSSEPKDRSPFOECLPKTDEVFQ 289
QY 287 PFYLSQLESVEEDYKSLKKEYSNENAVYKRMOSTLOLDCVAVPSSRSNATBOPSLHSS 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 290 -----MVENNMAAAVSTVKDFLSQLRSSNRRF-----SIPES----- 321
QY 347 QGLGMPVEESWFAVSLHPOEENE-----PSL--OSKLODE 381
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 --GGGTMDGFRRTIENQHSRNDVWVSEWLKLNLEPPSSVPRKCPSLTKRSRAOEE 378

```

```

QY 382 ANYHLGSRMDROTQOOPRQ 401
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 379 QVPOAMTAGTSSDMAOPQ 398

```

```

Query Match 11.7%; Score 414; DB 4; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-26;
Matches 124; Conservative 77; Mismatches 129; Indels 110; Gaps 16;

```

```

QY 14 SSDPLESAEL-DSGGFGKVSICFHRTQGLMIMKTYKGPNCIEHNEALLEAKMNRRLH 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 17 STEELNDELVGKGGFGVFRQHRKMG-----YDVAVKIVNSKAISREVKAMASLDN 69
QY 73 SRVVKLLGVITIEG-----KYSLVMEYMEKGNLMHVAKAMSTPLSVKGRITILEIEGM 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 EFLVRLFGVIEKVGSSODPKPALVTKFEMENGLSLGLOSOCPPRPWPLLCRLKEVVLGM 129
QY 127 CYLHGKG--VIHKDLKPNILVNDNFIKIDGLASFKMMSKLNNEHNEHLREVDTAK 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 FYLHDQNPVLLHRDLKPSNVLLDPELHVKLADFGISTFGGSGQ-----SGTGS 177
QY 185 -KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKE---PYE-----NAICEQ 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 GEGGGLGYLAPLEFVNNRKAStADSVYSGILMAYVLAGEVELPTEPSLYEAVCNR 237
QY 236 OLIMCKSGNRPDVIDITEYCPRE-----IISLKLCEANPEARPTF---PGLIEKFR 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 Q-----NPSLAELPQAGPETPGLGLEKELMQLCWSSEPKDRSPFOECLPKTDEVFQ 289
QY 287 PFYLSQLESVEEDYKSLKKEYSNENAVYKRMOSTLOLDCVAVPSSRSNATBOPSLHSS 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 290 -----MVENNMAAAVSTVKDFLSQLRSSNRRF-----SIPES----- 321
QY 347 QGLGMPVEESWFAVSLHPOEENE-----PSL--OSKLODE 381
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 --GGGTMDGFRRTIENQHSRNDVWVSEWLKLNLEPPSSVPRKCPSLTKRSRAOEE 378

```

Search completed: June 21, 2003, 16:16:12
 Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2003, 16:14:55 ; Search time 113 Seconds
(without alignments)
1521.290 Million cell updates/sec

Title: US-09-981-397A-16
Perfect score: 3545
Sequence: 1 MOPDMSLVNVIKMKSSDFLES.....ALHOCSDRLDLSLLIYQSN 671

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1160474 seqs, 256193413 residues

Total number of hits satisfying chosen parameters: 1160474

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCIT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3541	99.9	671	7	US-60-443-566-4422 Sequence 4422, Ap
2	3541	99.9	671	7	US-60-452-680-20110 Sequence 20110, A
3	3541	99.9	671	7	US-60-455-444-6356 Sequence 6356, Ap
4	3541	99.9	671	7	US-60-465-241-6356 Sequence 6356, Ap
5	3541	99.9	821	7	US-60-443-566-4424 Sequence 4424, Ap
6	3541	99.9	821	7	US-60-452-680-20112 Sequence 20112, A
7	3541	99.9	821	7	US-60-455-444-6358 Sequence 6358, Ap
8	3541	99.9	821	7	US-60-465-241-6358 Sequence 6358, Ap
9	3204	90.4	606	7	US-60-443-566-4423 Sequence 4423, Ap
10	3204	90.4	606	7	US-60-452-680-20111 Sequence 20111, A
11	3204	90.4	606	7	US-60-455-444-6357 Sequence 6357, Ap
12	3204	90.4	606	7	US-60-465-241-6357 Sequence 6357, Ap
13	1803	50.9	406	5	US-09-724-676-69182 Sequence 69182, A
14	1803	50.9	406	5	US-09-724-676-69182 Sequence 69182, A
15	1055	29.8	256	5	US-09-724-676-69183 Sequence 69183, A
16	1055	29.8	256	5	US-09-724-676-69183 Sequence 69183, A
17	433.5	12.2	555	5	US-09-949-016-10660 Sequence 10660, A
18	433	12.2	518	7	US-60-443-566-2658 Sequence 2658, Ap
19	433	12.2	518	7	US-60-455-444-80711 Sequence 80711, Ap
20	433	12.2	518	7	US-60-465-241-80711 Sequence 80711, Ap
21	419.5	11.8	786	1	PCT-US03-12676-33 Sequence 33, Appl
22	414.5	11.7	650	7	US-60-443-566-2657 Sequence 2657, Ap
23	414.5	11.7	650	7	US-60-455-444-8070 Sequence 8070, Ap
24	414.5	11.7	650	7	US-60-465-241-8070 Sequence 8070, Ap
25	410.5	11.6	439	1	PCT-US03-12676-28 Sequence 28, Appl
26	410.5	11.6	786	1	PCT-US03-12676-13 Sequence 13, Appl

27	410.5	11.6	786	6	US-10-299-327-2	Sequence 2, Appl
28	406	11.5	77	6	US-10-287-594-7	Sequence 7, Appl
29	405.5	11.4	786	1	PCT-US03-12676-32	Sequence 32, Appl
30	402.5	11.4	786	1	PCT-US03-12676-31	Sequence 31, Appl
31	384	10.8	784	1	PCT-US03-02568-38	Sequence 38, Appl
32	384	10.8	784	1	PCT-US03-12676-12	Sequence 12, Appl
33	384	10.8	784	5	US-09-949-016-6974	Sequence 6974, Ap
34	384	10.8	784	6	US-10-258-951-70	Sequence 70, Appl
35	384	10.8	784	6	US-10-354-358-38	Sequence 38, Appl
36	384	10.8	784	7	US-60-452-680-23803	Sequence 23803, A
37	384	10.8	787	5	US-09-949-016-11076	Sequence 11076, A
38	375.5	10.6	765	1	PCT-US03-12676-43	Sequence 43, Appl
39	372.5	10.5	765	1	PCT-US03-12676-3	Sequence 3, Appl
40	372.5	10.5	765	1	PCT-US03-12676-44	Sequence 44, Appl
41	372.5	10.5	765	6	US-10-285-325-2	Sequence 2, Appl
42	371.5	10.5	786	1	PCT-US03-12676-27	Sequence 27, Appl
43	371.5	10.5	765	1	PCT-US03-12676-36	Sequence 36, Appl
44	371.5	10.5	765	1	PCT-US03-12676-37	Sequence 37, Appl
45	371.5	10.5	765	1	PCT-US03-12676-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1									
US-60-443-566-4422									
Sequence 4422, Application US/60443566									
GENERAL INFORMATION:									
APPLICANT: CARGILL, Michele									
APPLICANT: BEGOVICH, Ann									
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH									
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF									
FILE REFERENCE: CLO01447									
CURRENT APPLICATION NUMBER: US/60/443,566									
CURRENT FILING DATE: 2003-01-30									
NUMBER OF SEQ ID NOS: 25102									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 4422									
LENGTH: 671									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-60-443-566-4422									
Query Match									
Best Local Similarity 99.9%: Score 3541; DB 7; Length 671;									
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	MOPDMSLVNVIKMKSSDFLES	AEIDSGGFGKYS	LCFHR	OGIMTKTVK	GPCIE	HNEL	60	
DB	1	MOPDMSLVNVIKMKSSDFLES	AEIDSGGFGKYS	LCFHR	OGIMTKTVK	GPCIE	HNEL	60	
QY	61	LEEAAMNRLRHSRVYKLLGV	IIIEGKYS	SLVMEY	EKGNLMHVL	KAENST	PLSVGR	120	
DB	61	LEEAAMNRLRHSRVYKLLGV	IIIEGKYS	SLVMEY	EKGNLMHVL	KAENST	PLSVGR	120	
QY	61	LEEAAMNRLRHSRVYKLLGV	IIIEGKYS	SLVMEY	EKGNLMHVL	KAENST	PLSVGR	120	
DB	61	LEEAAMNRLRHSRVYKLLGV	IIIEGKYS	SLVMEY	EKGNLMHVL	KAENST	PLSVGR	120	
QY	121	ETIEECMYLHGKGVTHKDL	KPENIL	LVND	PHIKIAD	ILGLASF	KMSKLN	NEENEL	180
DB	121	ETIEECMYLHGKGVTHKDL	KPENIL	LVND	PHIKIAD	ILGLASF	KMSKLN	NEENEL	180
QY	121	ETIEECMYLHGKGVTHKDL	KPENIL	LVND	PHIKIAD	ILGLASF	KMSKLN	NEENEL	180
DB	121	ETIEECMYLHGKGVTHKDL	KPENIL	LVND	PHIKIAD	ILGLASF	KMSKLN	NEENEL	180
QY	181	GTAKNGGTLVYMADEH	LDVNAK	PTEKSD	VSFAV	VMAT	PANKEP	ENALICE	240
DB	181	GTAKNGGTLVYMADEH	LDVNAK	PTEKSD	VSFAV	VMAT	PANKEP	ENALICE	240
QY	241	IKSGNRPPVDITTEY	CPREIIS	SLMKLC	WEANPEAR	PTEGIE	KRRPYL	LSOLE	300
DB	241	IKSGNRPPVDITTEY	CPREIIS	SLMKLC	WEANPEAR	PTEGIE	KRRPYL	LSOLE	300
QY	301	VKSLLKEKSENAAYV	KMQSI	QLDC	VAVP	SSNS	SNAT	EQPS	360
DB	301	VKSLLKEKSENAAYV	KMQSI	QLDC	VAVP	SSNS	SNAT	EQPS	360
QY	361	PSLIEHPQENERS	LOS	KODE	ANVYL	YGRMD	ROTK	QOP	420
DB	361	PSLIEHPQENERS	LOS	KODE	ANVYL	YGRMD	ROTK	QOP	420
QY	420	PSLIEHPQENERS	LOS	KODE	ANVYL	YGRMD	ROTK	QOP	420
DB	420	PSLIEHPQENERS	LOS	KODE	ANVYL	YGRMD	ROTK	QOP	420

```

Db      361 PSLEHPOEENPSLOSLODEANHYLHYSGRMDROTQOPRONAVAYNEEERRRVSHDP 420
Qy      421 AOOPEYENFONTEGKGTAVSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFGRPLD 480
      421 AOOPEYENFONTEGKGTAVSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFGRPLD 480
Db      421 AOOPEYENFONTEGKGTAVSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFGRPLD 480
Qy      481 PSTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
      481 PSTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
Db      481 PSTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
Qy      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHKMN 600
      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHKMN 600
Db      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHKMN 600
Qy      601 CARLGFQTSQIDEIDHDERDGLKEKYOMLOKWMREGIKGATVGKLAQALHOCSTRID 660
      601 CARLGFQTSQIDEIDHDERDGLKEKYOMLOKWMREGIKGATVGKLAQALHOCSTRID 660
Db      601 CARLGFQTSQIDEIDHDERDGLKEKYOMLOKWMREGIKGATVGKLAQALHOCSTRID 660
Qy      661 LLSSLIYVSQN 671
      661 LLSSLIYVSQN 671
Db      661 LLSSLIYVSQN 671

RESULT 2
US-60-452-680-20110
; Sequence 20110, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GROPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 20110
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-20110

```

```

Query Match      99.9%; Score 3541; DB 7; Length 671;
Best Local Similarity 99.9%; Pred. No. 4,2e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MOPDMSLVNIKMKSSDPLESAELDSGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
      1 MOPDMSLVNIKMKSSDPLESAELDSGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
Db      1 MOPDMSLVNIKMKSSDPLESAELDSGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
Qy      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
Db      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
Qy      121 EIIEGMCYLHGKGYIHKDLKRENILVNDPHIKIADGLASFKMKSKLNNEHNELREVD 180
      121 EIIEGMCYLHGKGYIHKDLKRENILVNDPHIKIADGLASFKMKSKLNNEHNELREVD 180
Db      121 EIIEGMCYLHGKGYIHKDLKRENILVNDPHIKIADGLASFKMKSKLNNEHNELREVD 180
Qy      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMAIFANKEPEYENALICEQOLIMC 240
      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMAIFANKEPEYENALICEQOLIMC 240
Db      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMAIFANKEPEYENALICEQOLIMC 240
Qy      241 IKSGRNPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSOLEESVEED 300
      241 IKSGRNPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSOLEESVEED 300
Db      241 IKSGRNPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSOLEESVEED 300
Qy      301 VKSLKKEYSNENAVYKRMQSLOLDCVAVPSSRSNSATEQPGSLHSSOGLMGVPEESWFA 360
      301 VKSLKKEYSNENAVYKRMQSLOLDCVAVPSSRSNSATEQPGSLHSSOGLMGVPEESWFA 360
Db      301 VKSLKKEYSNENAVYKRMQSLOLDCVAVPSSRSNSATEQPGSLHSSOGLMGVPEESWFA 360
Qy      361 PSLEHPOEENPSLOSLODEANHYLHYSGRMDROTQOPRONAVAYNEEERRRVSHDP 420
      361 PSLEHPOEENPSLOSLODEANHYLHYSGRMDROTQOPRONAVAYNEEERRRVSHDP 420
Db      361 PSLEHPOEENPSLOSLODEANHYLHYSGRMDROTQOPRONAVAYNEEERRRVSHDP 420

```

```

Qy      421 AOOPEYENFONTEGKGTAVSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFGRPLD 480
      421 AOOPEYENFONTEGKGTAVSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFGRPLD 480
Db      421 AOOPEYENFONTEGKGTAVSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFGRPLD 480
Qy      481 PSTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
      481 PSTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
Db      481 PSTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
Qy      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHKMN 600
      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHKMN 600
Db      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHKMN 600
Qy      601 CARLGFQTSQIDEIDHDERDGLKEKYOMLOKWMREGIKGATVGKLAQALHOCSTRID 660
      601 CARLGFQTSQIDEIDHDERDGLKEKYOMLOKWMREGIKGATVGKLAQALHOCSTRID 660
Db      601 CARLGFQTSQIDEIDHDERDGLKEKYOMLOKWMREGIKGATVGKLAQALHOCSTRID 660
Qy      661 LLSSLIYVSQN 671
      661 LLSSLIYVSQN 671
Db      661 LLSSLIYVSQN 671

RESULT 3
US-60-455-444-6356
; Sequence 6356, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 6356
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-455-444-6356

```

```

Query Match      99.9%; Score 3541; DB 7; Length 671;
Best Local Similarity 99.9%; Pred. No. 4,2e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MOPDMSLVNIKMKSSDPLESAELDSGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
      1 MOPDMSLVNIKMKSSDPLESAELDSGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
Db      1 MOPDMSLVNIKMKSSDPLESAELDSGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
Qy      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
Db      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
Qy      121 EIIEGMCYLHGKGYIHKDLKRENILVNDPHIKIADGLASFKMKSKLNNEHNELREVD 180
      121 EIIEGMCYLHGKGYIHKDLKRENILVNDPHIKIADGLASFKMKSKLNNEHNELREVD 180
Db      121 EIIEGMCYLHGKGYIHKDLKRENILVNDPHIKIADGLASFKMKSKLNNEHNELREVD 180
Qy      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMAIFANKEPEYENALICEQOLIMC 240
      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMAIFANKEPEYENALICEQOLIMC 240
Db      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSFAVYLMAIFANKEPEYENALICEQOLIMC 240
Qy      241 IKSGRNPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSOLEESVEED 300
      241 IKSGRNPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSOLEESVEED 300
Db      241 IKSGRNPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSOLEESVEED 300
Qy      301 VKSLKKEYSNENAVYKRMQSLOLDCVAVPSSRSNSATEQPGSLHSSOGLMGVPEESWFA 360
      301 VKSLKKEYSNENAVYKRMQSLOLDCVAVPSSRSNSATEQPGSLHSSOGLMGVPEESWFA 360
Db      301 VKSLKKEYSNENAVYKRMQSLOLDCVAVPSSRSNSATEQPGSLHSSOGLMGVPEESWFA 360
Qy      361 PSLEHPOEENPSLOSLODEANHYLHYSGRMDROTQOPRONAVAYNEEERRRVSHDP 420
      361 PSLEHPOEENPSLOSLODEANHYLHYSGRMDROTQOPRONAVAYNEEERRRVSHDP 420
Db      361 PSLEHPOEENPSLOSLODEANHYLHYSGRMDROTQOPRONAVAYNEEERRRVSHDP 420

```

```
QY 421 AAOBPYENFONTECKGTAYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
      |||||||
Db 421 AAOBPYENFONTECKGTAYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
QY 481 PGTAGPRVWTRPIPSHMSPLHNIPVETNVLGNTPMPFSSLPPTDESIKTYTINSIGIO 540
      |||||||
Db 481 PGTAGPRVWTRPIPSHMSPLHNIPVETNVLGNTPMPFSSLPPTDESIKTYTINSIGIO 540
QY 541 IGAVNMEIGTSSSLDSTNTNFKKEPPAKYOAIFONTTSLTDKHLDP1RENLGKHMKN 600
      |||||||
Db 541 IGAVNMEIGTSSSLDSTNTNFKKEPPAKYOAIFONTTSLTDKHLDP1RENLGKHMKN 600
QY 601 CARLGTQSQIDEIDHDYERDGLKEKVVOMLQKWVREGIKGATVGLAQAALHQCSTRID 660
      |||||||
Db 601 CARLGTQSQIDEIDHDYERDGLKEKVVOMLQKWVREGIKGATVGLAQAALHQCSTRID 660
QY 661 LLSLIYVSON 671
      |||||||
Db 661 LLSLIYVSON 671
```

RESULT 4

```
US-60-465-241-6356
: Sequence 6356, Application US/60465241
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: BEGOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: C1001468
: CURRENT APPLICATION NUMBER: US/60/465, 241
: CURRENT FILING DATE: 2003-04-23
: NUMBER OF SEQ. ID NOS: 258418
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 6356
: LENGTH: 671
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-465-241-6356
```

Query Match 99.9%: Score 3541; DB 7; Length 671;
Best Local Similarity 99.9%: Pred. No. 4.2e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MOPDMSLVITKMKSSDFLESABLDSDGGFGKVSICFHRTOGLMTKTYKGPNCIEHNEAL 60
      |||||||
Db 1 MOPDMSLVITKMKSSDFLESABLDSDGGFGKVSICFHRTOGLMTKTYKGPNCIEHNEAL 60
QY 61 LEEAKMMNRLRHSRVVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
      |||||||
Db 61 LEEAKMMNRLRHSRVVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
QY 121 EIIIEGMCYLGKGVIAHKDLKPENLVDNDFHIKTIADGLASFWMKSKLNNEHNEALREV 180
      |||||||
Db 121 EIIIEGMCYLGKGVIAHKDLKPENLVDNDFHIKTIADGLASFWMKSKLNNEHNEALREV 180
QY 181 GTAKKNGCTLYYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKKEYENAIICQOOLIMC 240
      |||||||
Db 181 GTAKKNGCTLYYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKKEYENAIICQOOLIMC 240
QY 241 IKSNGRPDVIDITEYCPREITISLMKLCMEANPEARPTFGIEEKFREFYLSOLEEVEED 300
      |||||||
Db 241 IKSNGRPDVIDITEYCPREITISLMKLCMEANPEARPTFGIEEKFREFYLSOLEEVEED 300
QY 301 VKSLKKEYSNEANVVKRMOSLQDCAVAPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 360
      |||||||
Db 301 VKSLKKEYSNEANVVKRMOSLQDCAVAPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 360
QY 361 PSLEHPOEENPESLOSLODEANVHLXGSRMDROTQKQPRONAVYNEEERRRRVSHDPF 420
      |||||||
Db 361 PSLEHPOEENPESLOSLODEANVHLXGSRMDROTQKQPRONAVYNEEERRRRVSHDPF 420
QY 421 AAOBPYENFONTECKGTAYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
      |||||||
```

```
Db 421 AAOBPYENFONTECKGTAYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
      |||||||
QY 481 PGTAGPRVWTRPIPSHMSPLHNIPVETNVLGNTPMPFSSLPPTDESIKTYTINSIGIO 540
      |||||||
Db 481 PGTAGPRVWTRPIPSHMSPLHNIPVETNVLGNTPMPFSSLPPTDESIKTYTINSIGIO 540
QY 541 IGAVNMEIGTSSSLDSTNTNFKKEPPAKYOAIFONTTSLTDKHLDP1RENLGKHMKN 600
      |||||||
Db 541 IGAVNMEIGTSSSLDSTNTNFKKEPPAKYOAIFONTTSLTDKHLDP1RENLGKHMKN 600
QY 601 CARLGTQSQIDEIDHDYERDGLKEKVVOMLQKWVREGIKGATVGLAQAALHQCSTRID 660
      |||||||
Db 601 CARLGTQSQIDEIDHDYERDGLKEKVVOMLQKWVREGIKGATVGLAQAALHQCSTRID 660
QY 661 LLSLIYVSON 671
      |||||||
Db 661 LLSLIYVSON 671
```

RESULT 5

```
US-60-443-566-4424
: Sequence 4424, Application US/60443566
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: BEGOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: C1001447
: CURRENT APPLICATION NUMBER: US/60/443, 566
: CURRENT FILING DATE: 2003-01-30
: NUMBER OF SEQ. ID NOS: 25102
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 4424
: LENGTH: 821
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-443-566-4424
```

Query Match 99.9%: Score 3541; DB 7; Length 821;
Best Local Similarity 99.9%: Pred. No. 5.5e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MOPDMSLVITKMKSSDFLESABLDSDGGFGKVSICFHRTOGLMTKTYKGPNCIEHNEAL 60
      |||||||
Db 151 MOPDMSLVITKMKSSDFLESABLDSDGGFGKVSICFHRTOGLMTKTYKGPNCIEHNEAL 210
QY 61 LEEAKMMNRLRHSRVVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
      |||||||
Db 211 LEEAKMMNRLRHSRVVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 270
QY 121 EIIIEGMCYLGKGVIAHKDLKPENLVDNDFHIKTIADGLASFWMKSKLNNEHNEALREV 180
      |||||||
Db 271 EIIIEGMCYLGKGVIAHKDLKPENLVDNDFHIKTIADGLASFWMKSKLNNEHNEALREV 330
QY 181 GTAKKNGCTLYYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKKEYENAIICQOOLIMC 240
      |||||||
Db 331 GTAKKNGCTLYYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKKEYENAIICQOOLIMC 390
QY 241 IKSNGRPDVIDITEYCPREITISLMKLCMEANPEARPTFGIEEKFREFYLSOLEEVEED 300
      |||||||
Db 391 IKSNGRPDVIDITEYCPREITISLMKLCMEANPEARPTFGIEEKFREFYLSOLEEVEED 450
QY 301 VKSLKKEYSNEANVVKRMOSLQDCAVAPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 360
      |||||||
Db 451 VKSLKKEYSNEANVVKRMOSLQDCAVAPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 510
QY 361 PSLEHPOEENPESLOSLODEANVHLXGSRMDROTQKQPRONAVYNEEERRRRVSHDPF 420
      |||||||
Db 511 PSLEHPOEENPESLOSLODEANVHLXGSRMDROTQKQPRONAVYNEEERRRRVSHDPF 570
QY 421 AAOBPYENFONTECKGTAYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
      |||||||
```

Db 571 A00RYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTRPLD 630
QY 481 PGTAGPRWYRPIPSHMPSLNINIPVETNYLGNPTMPFSSLPPTDESIXTYINSTG10 540
Db 631 PGTAGPRWYRPIPSHMPSLNINIPVETNYLGNPTMPFSSLPPTDESIXTYINSTG10 690
QY 541 IGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDMNTSLTDKHLDP1REN1GKHKMN 600
Db 691 IGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDMNTSLTDKHLDP1REN1GKHKMN 750
QY 601 CARLIGFTQSOQIDELDH0YERDGLKEKYOMLQKWMBEGIKGATVGLA0ALH0CSRID 660
Db 751 CARLIGFTQSOQIDELDH0YERDGLKEKYOMLQKWMBEGIKGATVGLA0ALH0CSRID 810
QY 661 LLSLIYVSQN 671
Db 811 LLSLIYVSQN 821

RESULT 6
US-60-452-680-20112
: Sequence 20112, Application US/60452680
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: GROPE, Andrew
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01450
: CURRENT APPLICATION NUMBER: US/60/452,680
: CURRENT FILING DATE: 2003-03-07
: NUMBER OF SEQ ID NOS: 116213
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 20112
: LENGTH: 821
: TYPE: PRF
: ORGANISM: Homo sapiens
US-60-452-680-20112

Query Match 99.9%; Score 3541; DB 7; Length 821;
Best Local Similarity 99.9%; Pred. No. 5.5e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPDMSLVNIYKSSDPLESAELDSGGFGKVSICFHRTQGLIMTKTYKGPNCIEHNEAL 60
Db 151 MOPDMSLVNIYKSSDPLESAELDSGGFGKVSICFHRTQGLIMTKTYKGPNCIEHNEAL 210
QY 61 LEEAKMNRRLNRSRVYKLLGVIIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Db 211 LEEAKMNRRLNRSRVYKLLGVIIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 270
QY 121 EIEGMCYLHGKGVITHKDLKPEINILVNDPFH1KIADLGLASFKMSKLNNEEHNELEVD 180
Db 271 EIEGMCYLHGKGVITHKDLKPEINILVNDPFH1KIADLGLASFKMSKLNNEEHNELEVD 330
QY 181 GTAKKNGGTLYYMAPEHNDVNAKPTKESDVYSFVAVYMA1FANKEPEENA1CE0QLIMC 240
Db 331 GTAKKNGGTLYYMAPEHNDVNAKPTKESDVYSFVAVYMA1FANKEPEENA1CE0QLIMC 390
QY 241 IKSGRNPVDDITECPRREIISLMKLCWEANPEARPTPG1EEKFRFPYLSQLEESVEED 300
Db 391 IKSGRNPVDDITECPRREIISLMKLCWEANPEARPTPG1EEKFRFPYLSQLEESVEED 450
QY 301 VKSLKKEYSNENAVVYKRM0SLQDLDCVAVPSSRSNSATB0PSGLSHSS0GLGMPVEESWFA 360
Db 451 VKSLKKEYSNENAVVYKRM0SLQDLDCVAVPSSRSNSATB0PSGLSHSS0GLGMPVEESWFA 510
QY 361 PSLEHPOEENESL0SKLQDEANHYLHYSRMDR0TK0Q0PR0NVAVYNNREERRRVSHDPF 420
Db 511 PSLEHPOEENESL0SKLQDEANHYLHYSRMDR0TK0Q0PR0NVAVYNNREERRRVSHDPF 570
QY 421 A00RYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTRPLD 480
Db 571 A00RYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTRPLD 630

QY 481 PGTAGPRWYRPIPSHMPSLNINIPVETNYLGNPTMPFSSLPPTDESIXTYINSTG10 540
Db 631 PGTAGPRWYRPIPSHMPSLNINIPVETNYLGNPTMPFSSLPPTDESIXTYINSTG10 690
QY 541 IGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDMNTSLTDKHLDP1REN1GKHKMN 600
Db 691 IGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDMNTSLTDKHLDP1REN1GKHKMN 750
QY 601 CARLIGFTQSOQIDELDH0YERDGLKEKYOMLQKWMBEGIKGATVGLA0ALH0CSRID 660
Db 751 CARLIGFTQSOQIDELDH0YERDGLKEKYOMLQKWMBEGIKGATVGLA0ALH0CSRID 810
QY 661 LLSLIYVSQN 671
Db 811 LLSLIYVSQN 821

RESULT 7
US-60-455-444-6358
: Sequence 6358, Application US/60455444
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: BEGOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01455
: CURRENT APPLICATION NUMBER: US/60/455,444
: CURRENT FILING DATE: 2003-03-18
: NUMBER OF SEQ ID NOS: 50986
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6358
: LENGTH: 821
: TYPE: PRF
: ORGANISM: Homo sapiens
US-60-455-444-6358

Query Match 99.9%; Score 3541; DB 7; Length 821;
Best Local Similarity 99.9%; Pred. No. 5.5e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPDMSLVNIYKSSDPLESAELDSGGFGKVSICFHRTQGLIMTKTYKGPNCIEHNEAL 60
Db 151 MOPDMSLVNIYKSSDPLESAELDSGGFGKVSICFHRTQGLIMTKTYKGPNCIEHNEAL 210
QY 61 LEEAKMNRRLNRSRVYKLLGVIIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Db 211 LEEAKMNRRLNRSRVYKLLGVIIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 270
QY 121 EIEGMCYLHGKGVITHKDLKPEINILVNDPFH1KIADLGLASFKMSKLNNEEHNELEVD 180
Db 271 EIEGMCYLHGKGVITHKDLKPEINILVNDPFH1KIADLGLASFKMSKLNNEEHNELEVD 330
QY 181 GTAKKNGGTLYYMAPEHNDVNAKPTKESDVYSFVAVYMA1FANKEPEENA1CE0QLIMC 240
Db 331 GTAKKNGGTLYYMAPEHNDVNAKPTKESDVYSFVAVYMA1FANKEPEENA1CE0QLIMC 390
QY 241 IKSGRNPVDDITECPRREIISLMKLCWEANPEARPTPG1EEKFRFPYLSQLEESVEED 300
Db 391 IKSGRNPVDDITECPRREIISLMKLCWEANPEARPTPG1EEKFRFPYLSQLEESVEED 450
QY 301 VKSLKKEYSNENAVVYKRM0SLQDLDCVAVPSSRSNSATB0PSGLSHSS0GLGMPVEESWFA 360
Db 451 VKSLKKEYSNENAVVYKRM0SLQDLDCVAVPSSRSNSATB0PSGLSHSS0GLGMPVEESWFA 510
QY 361 PSLEHPOEENESL0SKLQDEANHYLHYSRMDR0TK0Q0PR0NVAVYNNREERRRVSHDPF 420
Db 511 PSLEHPOEENESL0SKLQDEANHYLHYSRMDR0TK0Q0PR0NVAVYNNREERRRVSHDPF 570
QY 421 A00RYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTRPLD 480
Db 571 A00RYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTRPLD 630

Db 481 YMEIGTSSLLDSTNTNKEEPAKYAIFDNTTSLDKHLDPIRENIGKHKNCARL 540

QY 606 GFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIGATVGKLAQALHQCSTRIDLLSSL 665

Db 541 GFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIGATVGKLAQALHQCSTRIDLLSSL 600

QY 666 IYVSON 671

Db 601 IYVSON 606

RESULT 10

US-60-452-680-20111

Sequence 20111, Application US/60452680

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: GRUPE, Andrew

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: CLO01450

CURRENT APPLICATION NUMBER: US/60/452,680

CURRENT FILING DATE: 2003-03-07

NUMBER OF SEQ ID NOS: 116213

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 20111

LENGTH: 606

TYPE: PRT

ORGANISM: Homo sapiens

US-60-452-680-20111

Query Match 90.4%; Score 3204; DB 7; Length 606;

Best Local Similarity 99.8%; Pred. No. 3.1e-247;

Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 MMNRLRHSRVYKLGVIIEEGKYSLVMEYMEKGNLMHVLKAKMSTPLSVKRIILEIEG 125

Db 1 MMNRLRHSRVYKLGVIIEEGKYSLVMEYMEKGNLMHVLKAKMSTPLSVKRIILEIEG 60

QY 126 MCYLHGKGVTHKDLKPENILVNDNFHRIADLGSLASFWMKSKLNNEEHNEELREVDGTAKK 185

Db 61 MCYLHGKGVTHKDLKPENILVNDNFHRIADLGSLASFWMKSKLNNEEHNEELREVDGTAKK 120

QY 186 NGCTLYMAPHLNDVNAKPTKESDVYSFAVVLNAIFANKPEYENALICEOOLLICISGN 245

Db 121 NGCTLYMAPHLNDVNAKPTKESDVYSFAVVLNAIFANKPEYENALICEOOLLICISGN 180

QY 246 RPVDVITEYCPRREIISLMKLCWEANPEARPTFGIEEKFPRFYLSQLEESVEEDVSKL 305

Db 181 RPVDVITEYCPRREIISLMKLCWEANPEARPTFGIEEKFPRFYLSQLEESVEEDVSKL 240

QY 306 KEYSNENAVVRKMSQLODCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWEPASLEH 365

Db 241 KEYSNENAVVRKMSQLODCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWEPASLEH 300

QY 366 POENEPBSLOKLODEANVHLXGSRMDROTQOPRONVAYNREERERRRVSHPDFAOORP 425

Db 301 POENEPBSLOKLODEANVHLXGSRMDROTQOPRONVAYNREERERRRVSHPDFAOORP 360

QY 426 YENFONTEGKGTAVSSAASHGNAVHOPSGLTQPOVLXONNGLYSSHGFGRPLDPCGTAG 485

Db 361 YENFONTEGKGTAVSSAASHGNAVHOPSGLTQPOVLXONNGLYSSHGFGRPLDPCGTAG 420

QY 486 PRVWRPRLPSPHPSLHNIPVPEITNYLGNTPMPSSLPPTDESICKYITYNSTGQIGAYN 545

Db 421 PRVWRPRLPSPHPSLHNIPVPEITNYLGNTPMPSSLPPTDESICKYITYNSTGQIGAYN 480

QY 546 YMEIGTSSLLDSTNTNKEEPAKYAIFDNTTSLDKHLDPIRENIGKHKNCARL 605

Db 481 YMEIGTSSLLDSTNTNKEEPAKYAIFDNTTSLDKHLDPIRENIGKHKNCARL 540

QY 606 GFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIGATVGKLAQALHQCSTRIDLLSSL 665

Db 541 GFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIGATVGKLAQALHQCSTRIDLLSSL 600

QY 666 IYVSON 671

Db 601 IYVSON 606

RESULT 11

US-60-455-444-6357

Sequence 6357, Application US/60455444

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: BEGOVICH, Ann

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

FILE REFERENCE: CLO01455

CURRENT APPLICATION NUMBER: US/60/455,444

CURRENT FILING DATE: 2003-03-18

NUMBER OF SEQ ID NOS: 50986

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6357

LENGTH: 606

TYPE: PRT

ORGANISM: Homo sapiens

US-60-455-444-6357

Query Match 90.4%; Score 3204; DB 7; Length 606;

Best Local Similarity 99.8%; Pred. No. 3.1e-247;

Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 MMNRLRHSRVYKLGVIIEEGKYSLVMEYMEKGNLMHVLKAKMSTPLSVKRIILEIEG 125

Db 1 MMNRLRHSRVYKLGVIIEEGKYSLVMEYMEKGNLMHVLKAKMSTPLSVKRIILEIEG 60

QY 126 MCYLHGKGVTHKDLKPENILVNDNFHRIADLGSLASFWMKSKLNNEEHNEELREVDGTAKK 185

Db 61 MCYLHGKGVTHKDLKPENILVNDNFHRIADLGSLASFWMKSKLNNEEHNEELREVDGTAKK 120

QY 186 NGCTLYMAPHLNDVNAKPTKESDVYSFAVVLNAIFANKPEYENALICEOOLLICISGN 245

Db 121 NGCTLYMAPHLNDVNAKPTKESDVYSFAVVLNAIFANKPEYENALICEOOLLICISGN 180

QY 246 RPVDVITEYCPRREIISLMKLCWEANPEARPTFGIEEKFPRFYLSQLEESVEEDVSKL 305

Db 181 RPVDVITEYCPRREIISLMKLCWEANPEARPTFGIEEKFPRFYLSQLEESVEEDVSKL 240

QY 306 KEYSNENAVVRKMSQLODCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWEPASLEH 365

Db 241 KEYSNENAVVRKMSQLODCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWEPASLEH 300

QY 366 POENEPBSLOKLODEANVHLXGSRMDROTQOPRONVAYNREERERRRVSHPDFAOORP 425

Db 301 POENEPBSLOKLODEANVHLXGSRMDROTQOPRONVAYNREERERRRVSHPDFAOORP 360

QY 426 YENFONTEGKGTAVSSAASHGNAVHOPSGLTQPOVLXONNGLYSSHGFGRPLDPCGTAG 485

Db 361 YENFONTEGKGTAVSSAASHGNAVHOPSGLTQPOVLXONNGLYSSHGFGRPLDPCGTAG 420

QY 486 PRVWRPRLPSPHPSLHNIPVPEITNYLGNTPMPSSLPPTDESICKYITYNSTGQIGAYN 545

Db 421 PRVWRPRLPSPHPSLHNIPVPEITNYLGNTPMPSSLPPTDESICKYITYNSTGQIGAYN 480

QY 546 YMEIGTSSLLDSTNTNKEEPAKYAIFDNTTSLDKHLDPIRENIGKHKNCARL 605

Db 481 YMEIGTSSLLDSTNTNKEEPAKYAIFDNTTSLDKHLDPIRENIGKHKNCARL 540

QY 606 GFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIGATVGKLAQALHQCSTRIDLLSSL 665

Db 541 GFTOSQIDEIDHDYERDGLKEKYOMLOKWMREGIGATVGKLAQALHQCSTRIDLLSSL 600

QY 666 IYVSON 671

Db 601 IYVSON 606

RESULT 12
US-60-465-241-6357
: Sequence 6357, Application US/60465241
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: BEGOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: C1001468
: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
: CURRENT APPLICATION NUMBER: US/60/465, 241
: NUMBER OF SEQ ID NOS: 258418
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 6357
: LENGTH: 606
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-465-241-6357

Query Match
Best Local Similarity 90.4%; Score 3204; DB 7; Length 606;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 MMNRLRSRYVYKLLGVIIIEGKYSLYMEYMEKGNLMHVLKAEKSTPLSVKGRILLIEIEG 125
DB 1 MMNRLRSRYVYKLLGVIIIEGKYSLYMEYMEKGNLMHVLKAEKSTPLSVKGRILLIEIEG 60

QY 126 MCYIHKGVYHKDLKPEYILVNDNFHIKIDLGLASFKMSKLNNEEHNEIREVDTAKK 185
DB 61 MCYIHKGVYHKDLKPEYILVNDNFHIKIDLGLASFKMSKLNNEEHNEIREVDTAKK 120

QY 186 NGGLTYMAPRHLNDVNAKPTKESDYVSAFVYLWAFIRKPEYENALICEQOLIMCKISGN 245
DB 121 NGGLTYMAPRHLNDVNAKPTKESDYVSAFVYLWAFIRKPEYENALICEQOLIMCKISGN 180

QY 246 RPVDVITEXCPREIISLMKLCWEANPEARPTFGIEKFRFYLSQLEEVDEEYKSLK 305
DB 181 RPVDVITEXCPREIISLMKLCWEANPEARPTFGIEKFRFYLSQLEEVDEEYKSLK 240

QY 306 KEYSNENAVYKRMOSLDLCVAVPSSNSATTEQPGSLHSSQGLMGVPEESWAPSLIEH 365
DB 241 KEYSNENAVYKRMOSLDLCVAVPSSNSATTEQPGSLHSSQGLMGVPEESWAPSLIEH 300

QY 366 POENEPSSLOSKLDDENYHLYGSRMDROTQOPRONAVYREEEERRRVSHDPAOQRP 425
DB 301 POENEPSSLOSKLDDENYHLYGSRMDROTQOPRONAVYREEEERRRVSHDPAOQRP 360

QY 426 YENFQNTGKGTVYSSAASHGNNAVHOPSGLTSPQVLYQNNGLYSSHGFGTRPLDPGTAG 485
DB 361 YENFQNTGKGTVYSSAASHGNNAVHOPSGLTSPQVLYQNNGLYSSHGFGTRPLDPGTAG 420

QY 486 PRVYRPIPSHMPESLHNIIPVETNYLQNTPTMPFSSLPPTDESIRYTYTINSGIOIGAYN 545
DB 421 PRVYRPIPSHMPESLHNIIPVETNYLQNTPTMPFSSLPPTDESIRYTYTINSGIOIGAYN 480

QY 546 YMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKLDPIRENLGKHMKNCAKRL 605
DB 481 YMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKLDPIRENLGKHMKNCAKRL 540

QY 606 GFTQSOIDEIDHDYERDGLKEKYOMLQKWMREGIGATYGLKLAQLHQCSTRIDLLSSL 665
DB 541 GFTQSOIDEIDHDYERDGLKEKYOMLQKWMREGIGATYGLKLAQLHQCSTRIDLLSSL 600

QY 666 IYVSQN 671
DB 601 IYVSQN 606

RESULT 13
US-09-724-676-69182
: Sequence 69182, Application US/09724676
: GENERAL INFORMATION:

: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 69182
: LENGTH: 406
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-724-676-69182

Query Match
Best Local Similarity 100.0%; Score 1803; DB 5; Length 406;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SATEQPGSLHSSQGLMGVPEESWAPSLIEHPOENEPSSLOSKLDDENYHLYGSRMDRO 394
DB 70 SATEQPGSLHSSQGLMGVPEESWAPSLIEHPOENEPSSLOSKLDDENYHLYGSRMDRO 129

QY 395 TKOOPRONAVYANREEEERRRVSHDPAOQRPYENFQNTGKGTVYSSAASHGNNAVHOPSG 454
DB 130 TKOOPRONAVYANREEEERRRVSHDPAOQRPYENFQNTGKGTVYSSAASHGNNAVHOPSG 189

QY 455 LTSQPOVLYQNNGLYSSHGFGTRPLDPGTAGPRVYRPIPSHMPESLHNIIPVETNYLQNT 514
DB 190 LTSQPOVLYQNNGLYSSHGFGTRPLDPGTAGPRVYRPIPSHMPESLHNIIPVETNYLQNT 249

QY 515 PTMPFSSLPPTDESIRYTYTINSGIOIGAYNVMETIGSSSLDSTNTNFKKEEPAKYO 574
DB 250 PTMPFSSLPPTDESIRYTYTINSGIOIGAYNVMETIGSSSLDSTNTNFKKEEPAKYO 309

QY 575 IFDNTTSLTDKHLDPIRENLGKHMKNCAKRLGFTQSOIDEIDHDYERDGLKEKYOMLQK 634
DB 310 IFDNTTSLTDKHLDPIRENLGKHMKNCAKRLGFTQSOIDEIDHDYERDGLKEKYOMLQK 369

QY 635 WVMREGIGATYGLKLAQLHQCSTRIDLLSLIYVSQN 671
DB 370 WVMREGIGATYGLKLAQLHQCSTRIDLLSLIYVSQN 406

RESULT 14
US-09-724-676A-69182
: Sequence 69182, Application US/09724676A
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676A
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 69182
: LENGTH: 406
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-724-676A-69182

Query Match
Best Local Similarity 100.0%; Score 1803; DB 5; Length 406;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SATEQPGSLHSSQGLMGVPEESWAPSLIEHPOENEPSSLOSKLDDENYHLYGSRMDRO 394
DB 70 SATEQPGSLHSSQGLMGVPEESWAPSLIEHPOENEPSSLOSKLDDENYHLYGSRMDRO 129

QY 395 TKOOPRONAVYANREEEERRRVSHDPAOQRPYENFQNTGKGTVYSSAASHGNNAVHOPSG 454
DB 130 TKOOPRONAVYANREEEERRRVSHDPAOQRPYENFQNTGKGTVYSSAASHGNNAVHOPSG 189

QY 455 LTSQPOVLYQNNGLYSSHGFGTRPLDPGTAGPRVYRPIPSHMPESLHNIIPVETNYLQNT 514
DB 190 LTSQPOVLYQNNGLYSSHGFGTRPLDPGTAGPRVYRPIPSHMPESLHNIIPVETNYLQNT 249

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Db 190 LTSQPVLYXNNGLYSHGFGRPLDPTAGRWYRPIPSHMSLNIPVETNYLGNT 249
QY 515 PTMPFSSLPPTDESISKYTYINSTGIQIGAYNMEIGTSSSLDSTNTNFKKEPAKYQA 574
Db 250 PTMPFSSLPPTDESISKYTYINSTGIQIGAYNMEIGTSSSLDSTNTNFKKEPAKYQA 309
QY 575 IFDNTTSLTDKHLDPRENLGKHWKNCARKLGFTQSQIDETDHDYERDGLKEKYQMLQK 634
Db 310 IFDNTTSLTDKHLDPRENLGKHWKNCARKLGFTQSQIDETDHDYERDGLKEKYQMLQK 369
QY 635 WWMREGIKGATVYKLAQALHQCSTRIDLSSLIYVSQN 671
Db 370 WWMREGIKGATVYKLAQALHQCSTRIDLSSLIYVSQN 406
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RESULT 15
US-09-724-676-69183
; Sequence 69183, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69183
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-69183
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Query Match 29.8%; Score 1055; DB 5; Length 256;
Best Local Similarity 96.1%; Pred. No. 5, 1e-76;
Matches 197; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 467 GLYSSHGFGTRPLDPTAGRWYRPIPSHMSLNIPVETNYLGNTPTMPFSSLPPTD 526
Db 52 GYFIDSSVGTREPLDPTAGRWYRPIPSHMSLNIPVETNYLGNTPTMPFSSLPPTD 111
QY 527 ESIKTYTYNSTGIGIQAIFYMEIGTSSSLDSTNTNFKKEPAKYQAI FDNNTTSLTDKH 586
Db 112 ESIKTYTYNSTGIGIQAIFYMEIGTSSSLDSTNTNFKKEPAKYQAI FDNNTTSLTDKH 171
QY 587 LDPITRENLGKHWKNCARKLGFTQSQIDETDHDYERDGLKEKYQMLQKWWMREGIKGATV 646
Db 172 LDPITRENLGKHWKNCARKLGFTQSQIDETDHDYERDGLKEKYQMLQKWWMREGIKGATV 231
QY 647 GKLAQALHQCSTRIDLSSLIYVSQN 671
Db 232 GKLAQALHQCSTRIDLSSLIYVSQN 256
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Search completed: June 21, 2003, 16:24:18
Job time : 115 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: June 25, 2003, 19:49:40 ; Search time 4006 Seconds
(without alignments)
4874.684 Million cell updates/sec

Title: US-09-981-397A-16
Perfect score: 3545
Sequence: 1 MOPDMSLVNFKMSDFLES.....ALHQCRRIDLSLIYVSON 671

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=xlp
-Q/cgn2_1/USPFO.spool/US09981397/runat_21062003_134007_18432/app-query.fasta.1.839
-DB=GenDb1 -QFm=fastlap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09981397 @CGN_1_1_3745 @runat_21062003_134007_18432 -NCPU=6 -ICU=3
-NO_MMAP -LARGEDBTRY -NBS_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pt:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_or:*
21: em_ov:*
22: em_ov:*
23: em_ov:*
24: em_pat:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3545	100.0	2016	6 AR145196	AR145196 Sequence
2	3545	100.0	2617	6 AX429238	AX429238 Sequence
3	3545	100.0	2617	6 AX460995	AX460995 Sequence
4	3545	100.0	2617	6 HSU50062	HSU50062 Homo sapien
5	3529	99.5	2137	6 168123	168123 Sequence .16
6	3505	98.9	9687	6 AR165919	AR165919 Sequence
7	2423.5	68.4	2268	10 HSU25995	HSU25995 Mus. musculu
8	2423.5	68.4	2268	10 HSU25994	HSU25994 Human cell
9	1971	55.6	1240	9 AK096523	AK096523 Homo sapi
10	1753.5	49.5	2862	9 AK096523	AK096523 Homo sapi
11	1040	29.3	149546	6 HS40816	HS408163 Homo DNA
12	583.5	16.5	109832	2 AC120978	AC120978 Rattus no
13	583.5	16.5	150691	2 AC131143	AC131143 Rattus no
14	448	12.6	1873	6 AR105327	AR105327 Sequence
15	448	12.6	1873	6 AX067676	AX067676 Sequence
16	446	12.6	1557	6 AR105328	AR105328 Sequence
17	446	12.6	1557	6 AX067677	AX067677 Sequence
18	435	12.3	1557	6 AF156884	AF156884 Homo sapi
19	423.5	11.9	3876	9 AK027424	AK027424 Homo sapi
20	419.5	11.8	3879	9 HSA278016	AJ278016 Homo sapi
21	414.5	11.7	3882	9 AB047783	AB047783 Homo sapi
22	410.5	11.6	3559	10 AF302127	AF302127 Mus muscu
23	408.5	11.5	2015	6 AX400815	AX400815 Sequence
24	408.5	11.5	2015	6 AF036537	AF036537 Rattus no
25	405.5	11.4	1437	6 AX100029	AX100029 Sequence
26	405.5	11.4	1852	10 BC029210	BC029210 Mus muscu
27	402.5	11.4	1833	10 AF178953	AF178953 Mus muscu
28	397.5	11.2	2499	6 AX166548	AX166548 Sequence
29	396.5	11.2	2463	6 AF487541	AF487541 Dantio rer
30	374	10.6	1620	10 AF461040	AF461040 Mus muscu
31	374	10.6	1620	10 AF487539	AF487539 Mus muscu
32	371	10.5	1620	6 AR183235	AR183235 Sequence
33	371	10.5	1620	6 AR205635	AR205635 Sequence
34	371	10.5	1620	6 AX082201	AX082201 Sequence
35	371	10.5	1623	9 AF078530	AF078530 Homo sapi
36	371	10.5	1898	9 BC004553	BC004553 Homo sapi
37	371	10.5	1902	9 AF064824	AF064824 Homo sapi
38	371	10.5	1931	6 AR183234	AR183234 Sequence
39	371	10.5	1931	6 AR205634	AR205634 Sequence
40	371	10.5	1931	6 AX082199	AX082199 Sequence
41	371	10.5	2501	6 AX429236	AX429236 Sequence
42	371	10.5	2501	6 AF027706	AF027706 Homo sapi
43	371	10.5	2502	6 AR194318	AR194318 Sequence
44	369.5	10.4	2348	6 AX207411	AX207411 Sequence
45	369	10.4	2098	6 AB2777	AB2777 Sequence 2

RESULT 1

ALIGNMENTS

ARI45196
LOCUS ARI45196 2016 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6211337.
ACCESSION ARI45196
VERSION ARI45196.1 GI:15107063
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2016)
AUTHORS Baichwal, V.R., Huang, J., Hsu, H. and Goeddel, D.V.
TITLE RIP: novel human protein involved in tumor necrosis factor signal transduction
JOURNAL Patent: US 6211337-A 1 03-APR-2001;
FEATURES
source location/Qualifiers
1..2016
BASE COUNT 629 a 446 c 514 g 427 t
ORIGIN
Alignment Scores:
Pred. No.: 2.99e-233 Length: 2016
Score: 3545.00 Matches: 671
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Gaps: 0
Indels: 0
US-09-981-397A-16 (1-671) x ARI45196 (1-2016)
QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
Db 1 ATGCAGACGACATGCTCCTGTAATGTCATTAAGATGAATCCAGATCCTCTCGAGAGT 60
QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisArgThrGlnGly 40
Db 61 GCAGACTGGACAGCGAGGCTTTGGAGAGGTCTCTGTGTTCCACAGAACCCAGGGA 120
QY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnCysIleGluHisAsnGluAlaLeu 60
Db 121 CTCATGATCATGAAGAAGCTGTACAGGGGCCCAACTGCATTGAGCACAAGAGCCCTC 180
QY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGly 80
Db 181 TTGGAGGAGCGGAGATGATGAACAAGACTGAGACACGCCGCTGCTGAACTCTGGGC 240
QY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
Db 241 GTCATCATAGAGAGAGGAAGTACTCCCTGGTGTATGGATGACATGAGAGGCAACCTG 300
QY 101 MethIValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
Db 301 ATGCACGTGCTGAAGCGGAGATGATGATCTCCGCTTCTGTAAAGAGAGATATTTTG 360
QY 121 GluIleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
Db 361 GAAATCTTTGAGAGAAATGCTACTTACATGAAAGCGCGATACACAAGAACTGAG 420
QY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
Db 421 CCTAAATAATCTCTGTGTGATTAATGACTCCACATTAAGATGCGAGACTCTGGCTTGGC 480
QY 161 SerPheLysMetLysPheLysLeuAsnAsnGluLysHisAsnGluLeuArgGluValAsp 180
Db 481 TCCTTTAAGATGTGAGCAAACTGATTAATGAACAGACACATGAGCTGAGGAAAGTGAC 540
QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLysLeuAsnAsp 200
Db 541 GGCACCGCTAAGAGATGGCGCACCCCTACTACTACATGCGCCGAGACACTGAATGAC 600
QY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValAlaLeuTyrAla 220
Db 601 GTCAACGCAAGCCCAAGAGAGTGGATGTGTACAGCTTTGCTGTATGACTCTGGGCG 660

QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCys 240
Db 661 ATATTGGAAATAGAGACCATATGAATATCTATCTGTGACGCGACGATTGATATGTGC 720
QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
Db 721 ATAAATCTGGGAAACAGGCCAGATGTGATGACATCACTGATGACTGTGCCAAGAAAT 780
QY 261 IleSerLeuMetLysLeuGlyCysTyrGluAlaAsnProGluAlaArgProThrPheProGly 280
Db 781 ATCAGTCTCAGTAAGCTCTGTGGAGAACGGAATCCGGAAGCTCGCCGACATTTCTGCGC 840
QY 281 IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluIleAsp 300
Db 841 ATTGAGAAAAATTTAGCCCTTTTATTTATTTAAGTCATATTAGAGAAAGTGTAGAAAGAGAC 900
QY 301 ValLysSerLeuLysLysGlyTyrSerAsnGluAsnAlaValValLysArgMetGlnSer 320
Db 901 GTGAAGACTTTAAAGAAAGACTATTCAAACGAAATGACGCTTGAGAGAAATGCAGTCT 960
QY 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
Db 961 CTTCAACTTGTATGTGTGGCAGTACCTTCAAGCCGGTCAAAATTCAGCCACAGAACAGCT 1020
QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluIleTyrThrPheAla 360
Db 1021 GGTTCACCTGCACAGTCTCCAGAGGACTTGGATGGGTCTGTGGAGAGATCTGTGTGTCT 1080
QY 361 ProSerLeuGluHisProGlnGluLysAsnGluProSerLeuGlnSerLysLeuGlnAsp 380
Db 1081 CTTTCCTCGAGACCCACAGAGAGATGAGCCCGCTGACAGATAAATCTCCAGAC 1140
QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
Db 1141 GAAGCCAACTACCATCTTTATGGACGCCGATGACAGGACGACAGAAACACACCCACGA 1200
QY 401 GlnAsnValAlaTyrAsnArgGluGluLysArgArgArgValSerHisAspProPhe 420
Db 1201 CAGATGTGGCTTTCACACAGAGAGAGAGAAAGAGACGAGGTCTCCATGACCTTTT 1260
QY 421 AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSer 440
Db 1261 CCACAGCAAGACCTTTCAGAGAAATTTTCAGATATCAAGAGGAAAGGACACTGTTATTC 1320
QY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
Db 1321 AGTCAGCCAGTCATGTAATGTCAGTCCACAGCCCTCAGGCGTCACACCAACCTCAA 1380
QY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
Db 1381 GTACTGTATCAGAACATGATGATTAATAGCTACATGGCTTTGGAACAAGACCACTGGAT 1440
QY 481 ProGlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeu 500
Db 1441 CCAGAGACAGCAGGTCTCCAGAGTTGTGTACAGGCCAATTCCAAGTCAATATGCTAGTCTG 1500
QY 501 HisAsnIleProValProGluThrAsnTyrLeuGlnLysAsnThrProThrMetProPheSer 520
Db 1501 CATATATATCCAGTGTGAGACCACTATCTAGGAATACACCCACCAATGCAATTCAGC 1560
QY 521 SerLeuProProThrAspGluSerIleLysTyrThrIleLysAsnSerThrGlyIleGln 540
Db 1561 TCCCTGGCACCAAGATGATCATTAATAATATATCCATATACATATATGCTGCTTGCAG 1620
QY 541 IleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThr 560
Db 1621 ATTGAGCCTTACATATTTATGAGATGTGTGGCAGAGTTCATCATCAGTACTAGACAGACA 1680
QY 561 AsnThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
Db 1681 AATAGCAATCTCAAGAAGAGCCAGTGTGATGATACCAAGCTATCTTTGATATATACACT 1740

OY	581	serleuThrAspLysSHSleLeuAspProIleArgGluAsnLeuGlyLysSHSTriPlysAsn	600
Db	1741	AGCTGACGGATTAAACACCTTGACCCATCCAGGAAATCTGGGAAGACCTGGAAAAAC	1800
OY	601	CysAlaIArgLysLeuGlyPheThGlnSerGlnIleLeaspGluIleaspPHisAspTyGlu	620
Db	1801	TGTGCCCCCTAAACCTGGGCTTCACACAGCTCAGATTGATGAATTTGACCATGACTATGAG	1860
OY	621	ArgAspGlyLeuLysGlyLysValTyGlnMetLeuGlnLysSTriPValMetArgGluGly	640
Db	1861	CGAGATGAGACGAAAGAAAGAGTTTACAGATGCTCCAAAGGTGGTGATGAGGAAAGCC	1920
OY	641	IleLysGlyAlaThrValGlyLysLeuAlaIleAlaIleHisGlnCysSerArgIleasp	660
Db	1921	ATTAAGGAGGAGCCAGGTGGGGAACCTGGCCAGCGCCACAGATGTTCCAGATCGAC	1980
OY	661	LeuLeuSerSerLeuIleTyValSerGlnAsn	671
Db	1981	CTTCTGACAGCTTGATTTCAGTCAGCCAGAAC	2013
RESULT 2			
LOCUS	AX429238	2617 bp	DNA
DEFINITION	Sequence 15 from Patent EP1201765.		linear
ACCESSION	AX429238		
VERSION	AX429238.1	GI:21540549	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
Source			
BASE COUNT			
ORIGIN			
Alignment Scores:			
Pred. NO.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
DB:			
US-09-981-397A-16 (1-671) x AX429238 (1-2617)			
OY	1	MetGlnProAspMetSerLeuAsnValIleLysMetLysSerAspPheLeuGluSer	20
Db	1	ATGCAACACGACATGCTCCTTGAATGTCATTAAATGAATCAAGATCCAGATCTCTCGAGAGT	60
OY	21	AlaGluLeuAspSerGlyLysPheGlyLysValSerLeuCysPheHisArgThGlnGly	40
Db	61	GCAGAACTGGACACGCGAGGCTTTGGGAAAGTGTCTGTGTCTTCCACAGAACCCAGGGA	120
OY	41	LeuMetIleMetLysThValTyLysGlyProAsnCysIleGluHisAsnGluAlaLeu	60
Db	121	CTCATGATCAAGAAACAGCTGTACAGAGGCCCAACTGCATTGAGACACAGAGGCCCTC	180
OY	61	LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGly	80
Db	181	TTGGAGGAGCGGAGATGATGAACAGACTGAGACACACCGGCTGTGTAAGCTCCTGGGC	240
OY	81	ValIleIleGluGluGlyLysTySerLeuValMetGlyTyMetGluLysGlyAsnLeu	100
Db	241	GTCATCATAGAGGAAGGGAAGTACTCCTCTGTGTGATGAGGTACATGAGGAAGGGCAACTG	300

OY	101	MethsValIeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu	120
Db	301	ATGCACGCTGCTGGAAGCCCGAGATAGACTCTCCGCTTTCTGTAAGAAGAGATTAATTTTG	360
OY	121	GluIleIleIleGluGlyMetCysTyrLysIleIleGlySerGlyValIleHisLysAspLeuLys	140
Db	361	GAATTCATGTGAAGAGAAATGTGCTACTTACATGTGAAGAAGCGGTGATACCAAGACCTGAAG	420
OY	141	ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla	160
Db	421	CCTGAATAATATCCTGTTGTGTAATAAGACTTCCACATTAAGATCCGACAGACTTCGGCTTGCC	480
OY	161	SerPheLysMetIrrpSerLysLeuAsnAsnGluIuHisAsnGluLeuAsnGluValAsp	180
Db	481	TTCCTTTAAGATGTGGAGCAAACTAATATATCAAGACACATGAGCTGGAGGAAGTGCAC	540
OY	181	GlyThrAlaLysLysAsnGlyGlyThrLeuLysTyrMetAlaProGluHisLysAsnAsp	200
Db	541	GGCACCGGTAGAGAAATGGCGGACACCTGTACTACATAGGGCGCCGACACTGAATGAC	600
OY	201	ValAsnAlaLysProThrGluLysSerAspValLysSerPheAlaValValLeuTrpAla	220
Db	601	GTCAACGCAAGCCCAACAGACAGAACTCGGATGTACAGCTTGTCTGTAATCTCTGGGCG	660
OY	221	IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGluIleIleMetCys	240
Db	661	ATATTTTGCATTAAGAGACCCATGAAAATCTTCTGTGAGCAGCACATTGATATGTGC	720
OY	241	IleLysSerGlyAsnArgProAspValAspAspIleThrGluLysCysProArgGluIle	260
Db	721	ATAAATATGTGGAACAGGCGCAGATGTGGATGACATCATGACTGAGTCCGCCAAGAAATT	780
OY	261	IleSerLeuMetLysLeuCysTyrTrpGluAlaAsnProGluAlaArgProThrPheProGly	280
Db	781	ATCAGCTCCAGGAAGCTCTGCTGGGAAGCGAATCCGGAAGCTCGCGCACATTTCTTCGCG	840
OY	281	IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAsp	300
Db	841	ATTGACAGAAAATTTAGCGCTTTTATTTAATTAAGTCAATTAAGACGAAGTGTGAGAGAGAC	900
OY	301	ValLysSerLeuLysGlyLysSerAsnGluAsnAlaValValLysArgMetGlnSer	320
Db	901	GTGAAGAAGTTAAAGAAAGACTATTCAACCAAAATGCAGCTTGGAGAGAAATCCAGCTT	960
OY	321	LeuGluLeuAspCysValAlaValProSerSerArgSerAsnSerAlaIrrhGluGlnPro	340
Db	961	CTTCAACTGTATTTGTGGCAGTACTCTTCAACGCCGTCAAAATTGACGACAGAACACCTT	1020
OY	341	GlySerLeuHisSerSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAla	360
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OY	401	GlnAsnValAlaTyrAsnArgGluGluGluLysArgTrpArgValSerHisAspProPhe	420
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OY	421	AlaGlnGluArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValLysSer	440
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OY	441	SerAlaAlaSerHisGlyAsnAlaValAlaHisGlnProSerGlyLeuTrpSerGlnProGln	460
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LOCUS Sequence 1 from Patent WO0236148.
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VERSION AX460995.1 GI:21726224
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REFERENCE
AUTHORS 1
TITLE Tschoop,J and Holler,N.
JOURNAL Use of death receptor ligands or rip to initiate the
FEATURES non-caspase-dependent cell death and compounds for inhibition of
SOURCE the non-caspase-dependent cell death
Apotech Research and Development Ltd. (CH)
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REFERENCE
AUTHORS      Hsu H., Huang J., Shu H.B., Baichwal V. and Goeddel D.V.
TITLE      TNF-dependent recruitment of the protein kinase RIP to the TNF
JOURNAL      Immunity 4 (4), 387-396 (1996)
MEDLINE      96200892
PUBMED      8612133
REFERENCE
AUTHORS      Huang,J., Hsu,H., Baichwal,V.R. and Goeddel,D.V.
TITLE      Direct Submission
JOURNAL      Submitted (26-FEB-1996) Biology, Tularik Inc., 270 East Grand
Avenue, South San Francisco, CA 94080, USA
3 (bases 1 to 2617)
Huang,J., Hsu,H., Baichwal,V.R. and Goeddel,D.V.
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Submitted (18-AUG-1998) Biology, Tularik Inc., 270 East Grand
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Sequence update by submitter
On Aug 18, 1998 this sequence version replaced gi:1236942.
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ACCESSION 168123
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REFERENCE 1 (bases 1 to 2137)
AUTHORS Leder, P., Seed, B., Stanger, B. Z., Lee, T. -H. and Kim, E.
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QY 21 AlgluLeuaspserGlyLypheGlyLysValSerLeuGlyPheHisatGThrGlnGly 40
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QY 41 LeuMetIleMetLysThrValTyrLysGlyProaspCysIleGluHisasnGluAlaLeu 60
Db 121 CTCATGATCATGAAGACAGTGTACAGAGGGCCCACTGCATTTGAGCAGACAGAGCCCTC 180
QY 61 LeuGluGluAlaLysMetMetasnArgLeuArgHisSerArgValValLysLeuLeuGly 80
Db 181 TTGGAGAGGCGGAAGATGATGACAGACAGACACAGCCGGGTGTAAGCTCTGGGC 240
QY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
Db 241 GTCATCTATAGAGAGAGGAGTACTCCCTGCTGATGAGTACATGAGAGAGGCAACCTG 300
QY 101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
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QY 121 GluIleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
Db 361 GAATCTTTAAGAGAAATGCTCTACTTACATGGAAGAGCGGTGATACACAAGAGACTGAAG 420
QY 141 ProGluasnIleLeuValAspAsnPheHisIleLysIleAlaAspLeuGlyLeuAla 160
Db 421 CCTGAAATATCTCTGTTGTAATGACTTCCACATTAAGATCGAGACCTGGCCTTGGCC 480
QY 161 SerPheLysMetLysPheLysLeuAsnAsnGluGluHisasnGluLeuArgGluValAsp 180
Db 481 TCCGTTTAAGATGTGACCAACAAGTAATGAAGAGACACAATGAGCTGAGAGAAAGTGGAC 540
QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAsp 200
Db 541 GGCACCCCTAAGAAAGATGGCGGACCCCTACTACATGCGCGCCGAGCACTGAATGAC 600
QY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValIleLeuTrpAla 220
Db 601 GTCAACCAAGACCCACAGAGAACTCGAGATGTGTACAGCTTGTGTGATGACTTGGGCG 660
QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCys 240

Db 661 ATATTTCGAATAGAGAGCCATATGAAGAATGCTATCTGTAGAGAGGAGCTTGATATATGTC 720
QY 241 IleLysSerGlyAsnArgProaspValAspAspIleThrGluTyrCysProArgGluIle 260
Db 721 ATAAATCTGGGAACAGCCAGATGTGATGATCATCTAGTACTGCTCCCAAGAGAAATT 780
QY 261 IleSerLeuMetLysLeuGlyTyrPheGluAlaAspProGluAlaArgProThrPheProGly 280
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QY 281 IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValIleGluLysP 300
Db 841 ATTGAAGAAAATTTAGCCCTTTTATTATTAACTAATAGAGAACTGATGAAGAGACGAC 900
QY 301 ValLysSerLeuLysLysGlyTyrTyrSerAsnGluAsnAlaValValLysArgMetGlnSer 320
Db 901 GTGAAGAGTTTAAAGAAAGATATTCAAGCAAAATGCAGTTGTGAAGAGAAATGCAGCTCT 960
QY 321 LeuGluLeuaspCysValAlaIleValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
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QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerThrPheAla 360
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QY 361 ProSerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAsp 380
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QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
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QY 401 GlnAsnValAlaTyrAsnArgGluGluGluArgArgArgValSerHisAspProPhe 420
Db 1201 CAGATGTGCTTATACACAGAGAGAGAGAAAGAGAGCGAGGTCTCCATGACCCCTTTT 1260
QY 421 AlaGlnIleArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSer 440
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QY 441 SerAlaIleSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
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QY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
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QY 501 HisAsnIleProValProGluThrAsnTyrLeuGlnLysAsnThrProThrMetProPheSer 520
Db 1501 CATATATCCAGAGTCTGAGACCACTATCTAGGAATTTCTCCACCACTGCACTTACG 1560
QY 521 SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
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RESULT 6
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LOCUS Sequence 2 from patent US 6280937.
ACCESSION ARI65919
VERSION ARI65919.1 GI:16241007
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9687)
AUTHORS Luo, Y., Yu, P., Men. and Lorens, J.
TITLE Shuttle vectors
JOURNAL Patent: US 6280937-A 2-28-AUG-2001;
FEATURES
source location/qualifiers
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/organism="unknown"
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Score: 3505.00 Matches: 668
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 2
Query Match: 98.87% Indels: 1
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US-09-981-397a-16 (1-671) x ARI65919 (1-9687)
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Db 1194 GAAGTGCACAGCGGAGGCTTGGGAGAGTGTCTCTGTGTTCACAGAACCCAGGAGCTC 1253
QY 42 MetIleMetLysThrValTyrLysGlyProAsnGlyIleGluHisAsnGluAlaLeuLeu 61
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Db 1374 ATCATAGAGGAAAGGAGTACTCCCTGATGATGAGTAACATGAGAGGCAACCTGATG 1433
QY 102 HisValLeuLysAlaGlnMetSerThrProLeuSerValLysGlyArgIleIleLeuGlu 121
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QY 122 IleIleGluGluMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysPro 141

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Db 1553 GAAATATCTCTTGTGATTAATGACTTCCACATTAAGATCCGAGACCTCGCGCTTCC 1612
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QY 182 ThrAlaLysLysAsnGlyLysThrLeuTyrTyrMetAlaProGluHisLysAspVal 201
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Db 1793 TTTCCAAATTAAGAGCCATATGAATGCTATCTGTGAGCAGCAGTTGATTAATGTGATA 1852
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Db 1853 AAATCTGGGAAACAGCCAGATGCTGATGACATCACTAGTACTGCTCCCAAGAGAAATATC 1912
QY 262 SerLeuMetLysLeuGlyTyrGluAlaAsnProGluAlaArgProThrPheProGlyIle 281
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QY 282 GlnGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspVal 301
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Db 2093 CAAGCTGATTTGTGGCAGTACTTCAAGCCGGTCAATTCAGCCACAGAACACCTGGT 2152
QY 342 SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaPro 361
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Db 2393 CAGCAAAAGACCTTTCGAGAAATTTTCAGATATCAAGAGGAAAGGCACTGTTATTCAGT 2452
QY 442 AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGluVal 461
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QY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
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DB 2633 AATATCCAGTGCCTGAGACCACTATCTAGGAATATACCCACCACTCCCTTAGCTCC 2632
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OY 542 GlyAlaIleTyrAsnTyrMetGluIleGlyLysThrSerSerSerLeuLeuAspSerThrAsn 561
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OY 562 ThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSer 581
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OY 582 LeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTyrPlysAsnGly 601
DB 2873 CTGACGGATTAACACCTGACCCCAATCAGGAAATCTGGGAAAGCACTGGAATAACTGT 2932
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DB 2933 GCCCGTAACCTGGGCTTCACACAGCTCTCAGATTGATGAATTGACCATGACTATAGCGCA 2992
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OY 642 LysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAspLeu 661
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OY 662 LeuSerSerLeuIleTyrValSerGlnAsn 671
DB 3113 CTGAGCAGCTTGATTGATGCTACGACCAAGAC 3142

RESULT 7
168122
LOCUS 168122 2268 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 14 from patent US 5674734.
ACCESSION 168122
VERSION 168122.1 GI:2830244
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2268)
AUTHORS Leder, P., Seed, B., Stanger, B. Z., Lee, T. -H. and Kim, E.
TITLE Cell death protein
JOURNAL Patent: US 5674734-A 14 OCT-1997;
FEATURES
source Location/Organism
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BASE COUNT 719 a 491 c 576 g 482 t
ORIGIN

Alignment Scores:
Pred. No.: 1.55e-156 Length: 2268
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Percent Similarity: 80.21% Conservative: 70
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Query Match: 68.36% Indels: 17
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US-09-981-397a-16 (1-671) x 168122 (1-2268)

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DB 472 CCTGAGAAATATCTCGCTGATGCTGACTTTCACATTAAGATAGCCGATCTGTGGCT 531
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Db	1246	AGGAGAAATGAGGGCTTCCACACGAGAGAGAGAAAGAAACGAAAGCTCTCATGACCCC	1305
OY	420	PheIaGInGInaIgaProTyrgLlAspPheGInaSnhrGluGlyLysGlyThrValTyr	439
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OY	440	SerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnPro	459
Db	1366	CCCAGCACAAACGAGTCTGCAATTCGACGTGCACACAGCTGTCATGTCGACCAACCCAA	1422
OY	460	GlnValLeuTyrgLlnAsnSnglyLeuTygSerSerHisGlyPheGlyThrIraProLeu	479
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OY	500	LeuHisAsnIleProValProGluThrAsnTyrlLeuGlyAsnThrProThiMetProPhe	519
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Db	1864	GAAAGAGATGACGTCGAAAGAGAAAGATTACCAATGCTTCAGAAAGTGCGTATGCGGAA	1923
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RESULT	8
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LOCUS	MMU25995
DEFINITION	2268 bp mRNA linear ROD 24-MAY-1995
ACCESSION	M25995
VERSION	U25995.1 GI:829618
KEYWORDS	Fas; TNF receptor.
SOURCE	Mus musculus.
ORGANISM	Mus musculus.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2268)
AUTHORS	Stanger,B.Z., Leder,P., Lee,T.H., Kim,E. and Seed,B.
TITLE	RIP: a novel protein containing a death domain that interacts with Fas/Apo-1 (CD95) In yeast and causes cell death

JOURNAL Cell 81 (4), 513-523 (1995)
 MEDLINE 95277838
 PUBMED 7538908
 REFERENCE 2 (bases 1 to 2268)
 AUTHORS Stanger,B.Z.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAY-1995) Ben Z. Stanger, Genetics, Harvard Medical School, 200 Longwood Avenue, Boston, MA 02115, USA

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 /translation="MPPDMSLDNTKMASDLEKTDLDGGFGKSLCYARSHGFVLLKRYVTPRKAEYINENVLLDEGKMRLHLSRYVLLGLILEGNYSLMEYMEGNLMLVLRKIDVPLSLKGRITVEALEGMCYLDHKGVIHRLDKLPENILVDROFRIKIDLVASFKWSKLTKEKDKROKESVSTTKKNGGTLYVAPHELNDLNAPKPEKSDVSPGIVLMAIFAKKEPEYENTGEOPYICISGNRPNVEILTECPREITSLMERCOMAIPDRPTGIFEEPRRPYLSHPREEVEDVASLTKKEYDOSPYQRMSLDHCPVLPPSSNSDEPGSLSHSQGLQMPREEVSFSSPEYPODENDSVAKILOEASTAFGIFARKQTRQAPRONENAYNREEERKRVSHDPAQDRARENKLSAARGHSDSTYSIAYQOLSWATQVTPQVNNGLYNQHGEGTGTGVAPPNLSOMYSTYKTPVETNIPGSPPTMYFSGVADDLIKYTIIFNSSGIQIGNHMYMDVGLNSOPNNCKEESTRHQAIPIDNTSLTDELHPINENLGRMKNCARKLGFESQIDEIDHDYERDGLKEKYVQLQWLMBREGTAKVYGLKLAQALHQQCRIDLNLHLIRASQS"
 1469
 variation
 /gene="RIP"
 /note="apparent polymorphism resulting in a Thr vs Ile variation"
 /replacement="T"
 1623
 variation
 /gene="RIP"
 /note="silent polymorphism"
 /replacement="C"
 BASE COUNT 719 a 490 c 577 g 482 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.55e-156 Length: 2268
 Score: 2423.50 Matches: 469
 Percent Similarity: 80.218 Conservative: 70
 Best Local Similarity: 69.79% Mismatches: 116
 Query Match: 68.36% Indels: 17
 DB: 10 Gaps: 5

US-09-981-397A-16 (1-671) x MM025995 (1-2268)

OY 1 MetcLInProbspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGluSer 20
 Db 52 ATGCAACCAAGACATCTCTTGAGCAAAATTAAGATGGATCATCACTGCTGGAGAG 111
 OY 21 AlagLLeuLeuAspSerArgLysPheGlyLysValSerLeuLeuSerPheHisArgThrGlnGly 40
 Db 112 ACAGACCTACACACGAGGAGCTTGAGGAGAGGTGCTCTTGTTTACCAACAGAGCATGGA 171
 OY 41 LeuMetLleMetLysThrValTyrLysGlyProAsnGlySrlleGluHisAsnGluAlaLeu 60
 Db 172 TTGTGTCATCTCGAATAAAGATATACACAGAGGCCCAACCGCGCTGATGCATGAGGTTCTC 231
 OY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGly 80
 Db 232 TTGTGAAGAGGGGAGATGATGACAGCACTAGACACAGCTGAGTGGAGGCTACTAGGGC 291

[illegible]

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/gene="RIP"
<1..1119
/gene="RIP"
/function="Fas interacting protein; cell death"
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QVLYQNGLYSSHGEGTRPDPGAPGRVWRPISPMPSLHNPVETNYLGSPTM
PFSLPPTDESIXKTYIYNSTGIGIAGAYNMEIGTSSSLDSTNTNKEEPAKYQAI
FDNTSLTDKLDPIRENLGKMKNCARKIGFTQSOIDEIDHDYERDGLKEKYQMO
KMWREGIKATYKLAQALHQCRIIDLLSLIYVSON"

BASE COUNT 380 a 295 c 303 g 262 t
ORIGIN

Alignment Scores:
Pred. No.: 5.88e-126 Length: 1240
Score: 1971.00 Matches: 371
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.73% Mismatches: 0
Query Match: 55.60% Indels: 0
DB: 9 Gaps: 0

US-09-981-397a-16 (1-671) x HSU25994 (1-1240)

QY 300 AspyAllysSerLeuLysLysGlyTyrSerAsnGluAsnAlaValLysArgMetGln 319
DB 1 GACCTGAAGATTAAAGAAAGAGTATTCACCAAAATGCACTGTGAAAGAGATCGAC 60
QY 320 SerLeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnGln 339
DB 61 TCTCTTAACCTGATGTGTGTGGCAGTACCTCAAGCCGCTCAATTCAGCCACGAAACAG 120
QY 340 ProGlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGlnLysSerTrpPhe 359
DB 121 CTTGCTTCACTGCACAGATTCGCCAGGAGCTGGAGTGGGTCTCTGAGAGAGTCTGTGTTT 180
QY 360 AlaProSerLeuGlnHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGln 379
DB 181 GCTCTCTTCCCTGGGACCCACAGAAAGAGATGAGCCCGCTGCGAGAGTAAACTCCAA 240
QY 380 AspGluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnPro 399
DB 241 GACCAACCCCAACTTCTTTATGACGCCGCTGGACAGGACGAGCAACAGCAGACCC 300
QY 400 ArgGlnAsnValAlaTyrAsnArgGluGluGlnArgArgArgValSerHisAspPro 419
DB 301 AGACAGAAATGGGTACACAGAGAGAGAGAAAGAGAGAGAGGCTCCCATGACCT 360
QY 420 PheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyr 439
DB 361 TTTGACAGCAAGAACCTTACGAGAAATTTTCAGAAATACAGAGGAAAGCACACTTAT 420
QY 440 SerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnPro 459
DB 421 TTCAGTGCACGCACTGATGTAAAGCAGTGCACGACCATCAGGGCTCCACAGCAGCCT 480
QY 460 GlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeu 479
DB 481 CAAGTACTGTATCAGACAAATGATATATAGCTACACATGGCTTGGACACAGCAGCTG 540
QY 480 AspProGlyThrAlaGlyProAlaGlyValTrpTyrArgProIleProSerHisMetProSer 499
DB 541 GATTCACAGAACACAGGTCCAGAGTTGGTACAGGCAATTCACAAATCATATAGCTAGT 600
QY 500 LeuHisAsnIleProValProGluThrAsnTyrLeuGlnLysAsnThrProThrMetProPhe 519
|||||

DB 601 CTGCATATATCCAGTCCCTGAGACCAACTATCTAGAAATTCCTCCACCATCCATTC 660
QY 520 SerSerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyTle 539
DB 661 AGCTCTTGGCCACCAACAGATGAATCTATATAATATACCATATACATAGTACTGGCAT 720
QY 540 GlnIleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSer 559
DB 721 CAGATTGAGAGCTCAATTTATATGAGATGTTGGTGGACGAGGTTCATCATCTAGACAGC 780
QY 560 ThrAsnThrAsnPheLysGluGlnProAlaAlaLysTyrGlnAlaIlePheAspAsnThr 579
DB 781 ACAATATCGAACTTCAAGAGAGACCGCTGCTAGTACCAAGCTACTTGTGATTAACCC 840
QY 580 ThrSerLeuThrAspLysHisLeuAspProIleArgLysLysLeuGlnLysHisTrpLys 599
DB 841 ACTAGTGTGACGAGTAAACACCTGACCCCATATCGGAAATCTGGGAAAGCAGCTGAAA 900
QY 600 AsnCysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyr 619
DB 901 AACTGTCCTCCGTAAACTGGGCTTCACACAGTCTCATGATGATGAATTCACCATGACTAT 960
QY 620 GlnArgAspGlyLeuLysGlyLysValTyrGlnMetLeuGlnLysTrpValMetArgGlu 639
DB 961 GAGCGACATGACCTGAAAGAAAGAGTTTACCAGATGCTCCAAAAGTGGCGATGAGGAA 1020
QY 640 GlyIleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIle 659
DB 1021 GGCAATTAAGGAGAGCCAGCTGGGAGAGCTGAGCCAGGCGCTCCACAGATGTCAGAGATC 1080
QY 660 AspleuLeuSerSerLeuIleTyrValSerGlnAsn 671
DB 1081 GACCTTCTGACAGCTGATTTACGTACGACAGCAGAAC 1116
RESULT 10
AK096523
LOCUS 2862 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ39204 f1s, clone OCBBF2005476, highly similar
to SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-).
ACCESSION AK096523
VERSION 1
KEYWORDS Oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens fetal brain cDNA to mRNA, clone_11b:OCBBF2
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J.,
Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K.,
Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H.,
Kanda,K., Magatsuna,M., Murakawa,K., Kanehori,K., Sugiyama,A.,
Kawakami,B., Suzuki,Y., Sugano,S., Nagahara,K., Masuno,Y., Nagai,K.
and Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2862)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@ri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
Location/Qualifiers

FEATURES


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/db.xref="taxon.9606"
/clone="OCB2005476"
/clone_type="brain"
/clone_id="OCB2005476"
/dev_stage="fetal"
/note="Cloning vector: PM18SFL3"

BASE COUNT      797 a      669 c      699 g      697 t
ORIGIN

Alignment Scores:
Pred. No.:      1,31e-110      Length:      2862
Score:          1753.50      Matches:      337
Percent Similarity: 91.83%      Mismatches: 0
Best Local Similarity: 91.83%      Indels:      30
Query Match:      9      Gaps:      1

US-09-981-397A-16 (1-671) x AK096523 (1-2862)

OY      306  LysGluIyrSerAnGluAsnAlaValAlLysArgMetGlnSerLeuGlnLeuAspCys 325
      |||||||
Db      2  AAAAGAGATTCAAAAGAAATGCAGTTGTGAAGAGATGCAGTCTTCAACTGATGTTGT 61

OY      326  ValAlaValAlProSerSerArgSerAsnSerAlaThrGlnGlnProGlySerLeuHisSer 345
      |||||||
Db      62  GTGGCAGTACCTTAAGCGCGGTCAAAATTCACCAAGACAGCCCTGGTTCACCTCAGCAGT 121

OY      346  SerGlnGlyLeuGlnGlyMetGlyProValGlnGlnSerTrpPheAlaProSerLeuGlnHis 365
      |||||||
Db      122  TCCGAGGAGACTTGGATGGGTCTGTGTGAGAGAGTCTGGTGTGCTCCCTCCCTGGAGAGC 181

OY      366  ProGlnGlnGluAsnGlnProSerLeuGlnSerLeuGlnAspGluAlaAsnTrpHis 385
      |||||||
Db      182  CCACAAAGAGATGAGGCCAGCCCTCAGAGTAACTCCAAAGACGAAGCCCACTACCAT 241

OY      386  LeuTrpGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyr 405
      |||||||
Db      242  CTTTATGGCAGCCCATGAGCAGCAGCAGCAAGACGAGCCCAAGATGTGGCTTAC 301

OY      406  AsnArgGlnGlnGluArgArgArgValSerHisAspProPheAla-GlnGlnArgPr 425
      |||||||
Db      302  AACGAGAGAGGAGAAAGAGAGAGCGAGGTCTCCCATGACCTTTTGGACAG----- 353

OY      425  cTyrGlnAsnPhelGlnAsnThrGlnGlyLysGlyThrValTyrSerSerAlaAlaSerHi 445
      |||||||
Db      353  ----- 353

OY      445  sGlyAsnAlaValAlHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAs 465
      |||||||
Db      354  -----CCCTAAGGCGTCCACCAAGCCCAACTCAAGTACTGATACGAA 394

OY      465  nasGlnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAlaG1 485
      |||||||
Db      395  CAATGGATTATATAGCTCACATGGCTTTGGAACAAGCACTGATCCAGAGAACAGCAGG 454

OY      485  yProArgValTrpArgProIleProSerHisMetProSerLeuHisAsnIleProVa 505
      |||||||
Db      455  TCCGAGAGTTTGGTACAGGCCCAATTCCAAGCATATGCTGATGATAATATATCCAGT 514

OY      505  lProGlnThrAsnTrpLeuGlnAsnThrProThrMetProPheSerSerLeuProProTh 525
      |||||||
Db      515  GCCGAGACCAACACATATAGGAATACACCCACCATGCCATTCAGCTCTTCCACACAC 574

OY      525  rAspGlnSerTrpLeuTyrThrIleTyrAsnSerTrpGlyIleGlnIleGlyAlaTyrAs 545
      |||||||
Db      575  AGATGATATCTATAAATAATACATATACATAGTACAGTTCAGATTTGAGGCTTCAAA 634

OY      545  nTyrMetGlnIleGlyThrSerSerSerLeuLeuAspSerThrTrpAsnPhely 565
      |||||||
Db      635  TTTATATGAGAGATTGGTGGAGAGAGTTCATCATCTAGACAGCAAGAAATAGCAACTCAA 694

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OY      565  sGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSerLeuThrAspLy 585
      |||||||
Db      695  AGAAGAGCCAGCTGCTAAGTCCAAAGCTATTTGATATATCCACTACTGACAGCATAA 754

OY      585  sHisLeuAspProIleArgGluAsnLeuGlyLysHisTrpLysAsnGlyAlaArgLysLe 605
      |||||||
Db      755  ACACCTGGACCCATTCAGGGAAGAAATTCGGGAAGACAGTGGAAAGAACTGTCCCTAAACT 814

OY      605  uGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGluArgAspGlyLeuLy 625
      |||||||
Db      815  GGGCTTCACACAGCTCAGATTGATGAATTTGACCATGATGATGAGCGAGATGCATGAA 874

OY      625  sGluLysValTrpGlnMetLeuGlnLysTrpValMetArgGluGlyIleLysGlyAlaTh 645
      |||||||
Db      875  AGAAAGGTTTACAGATGCTTCCAAAAGTGGGTATGAGGAGGCAATAAAGGAGCCAC 934

OY      645  rValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgTrpIleAspLeuSerSerLe 665
      |||||||
Db      935  GGTGGGAGAGCTGGCCAGCGGCTCCACCACTGTTTCCAGATGTCAGACCTTTCAGACAGCTT 994

OY      665  uIleTyrValSerGlnAsn 671
      |||||||
Db      995  GATTTCAGTCAAGCCAGAAC 1013

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RESULT 11
LOCUS      HS40E16      149546 bp      DNA      linear      PRI 10-MAR-2001
DEFINITION Human DNA sequence from clone RPI-40E16 on chromosome 6p24.1-25.3,
ACCESSION AL031963
VERSION    AL031963.40 GI:13235084
KEYWORDS   HTS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
            1 (bases 1 to 149546)
REFERENCE 1
            Direct Submission
            Submitted (02-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
            requests: clonerequests@sanger.ac.uk
            On Mar 5, 2001 this sequence version replaced gi:13171042.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TrEMBL; Wp:, WormPep; information on the WormPep
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep
            This sequence was generated from part of bacterial clone contigs of human
            chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
            Group. Further information can be found at
            http://www.sanger.ac.uk/MGP/chr6
            RPI-40E16 is from the library RPI-1 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pCYPAC2
            This sequence is the entire insert of clone RPI-40E16 The true left
            end of clone RPI-112K15 is at 88226 in this sequence. The true
            right end of clone RPI-90J20 is at 9716 in this sequence.
            Location/Qualifiers

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FEATURES

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  /clone_lib="RPC1-1"
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      1192. .1244
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          1245. .1465
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                                                                                                          34756. .34799
                                                                                                            repeat_region
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                                                                                                              35472. .35579
                                                                                                                repeat_region
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                                                                                                                  35488. .35577
                                                                                                                    repeat_region
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                                                                                                                      35581. .35638
                                                                                                                        repeat_region
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                                                                                                                                repeat_region
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                                                                                                                                  36485. .36963
                                                                                                                                    repeat_region
                                                                                                                                      /note="L1MC2 repeat: matches 5603. .6111 of consensus"
                                                                                                                                      37058. .37373
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```

repeat_region 37522..37678
 /note="LIME2 repeat: matches 5428..5585 of consensus"
 repeat_region 38781..39092
 /note="AluJo repeat: matches 2..301 of consensus"
 repeat_region 39094..39119
 /note="13 copies 2 mer at 100% conserved"
 repeat_region 40455..40571

Alignment Scores:

Pred. No.: 1.44e-59 Length: 149546
 Score: 1040.00 Matches: 197
 Percent Similarity: 92.00% Conservative: 10
 Best Local Similarity: 87.56% Mismatches: 11
 Query Match: 29.34% Indels: 7
 DB: 9 Gaps: 2

US-09-981-397a-16 (1-671) x HS40E16 (1-149546)

OY 335 SerAlaThrGluGlnProGlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProVal 354
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 Db 67872 TCACCCACAGAACGCTGGTTCACGACGTTCCACGAGCCTGGGATGGCTCTGTG 67931
 OY 355 GluGlnSerTrpPheAlaProSerLeuGluHisProGlnGluGluAsnGluProSerLeu 374
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 Db 67932 GAGGAGTCTGGTTCCTCCCTCCGAGACCCACAGAACAGAAATGAGCCAGCCTG 67991
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 |||||
 Db 67992 CAGGTAACCTCCAGACGAAAGCCACATCCATCTTTATGGCAGCCGATGACAGCGAC 68051
 OY 395 ThrIleGlnGlnProGlnAsnValAlaTrpAsnArgGluGluGluArgArgArg 414
 |||||
 Db 68052 ACGAAGACGACGCCACAGACGAATGTGGCTTACACAGAGAGAGAGAAAGACGACGAG 68111
 OY 415 ValSerHisAspProPheAlaGlnGlnArgProTrpGluAsnGlnPheGlnAsnThrGluGly 434
 |||||
 Db 68112 GTCTCCCATGACCTTTTGGACACAGCAAGACCTTACGAGATTTTCAAGAAATACAGAGGA 68171
 OY 435 LysGlyThrValTrpSerSerAlaAlaSerHisGlyAsnAlaHisGlnProSerGly 454
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 Db 68172 AAAGGCACTGCTTATTCAGAGGACGACGATCATGTATGACGACGACCCCTCAGGC 68231
 OY 455 LeuThrSerGlnProGlnValLeuTrpGlnAsnAsnGlyLeuTrpSerSerHisGlyPhe 474
 |||||
 Db 68232 CTCACGACGACCACTCAAGTACTGATACAGAACATGATATATAGTCTCAATGCGCTT 68291
 OY 475 GlyThrArgProLeuAspProGlyThrAlaGlyProArgValTrpTrpArgProIlePro 494
 |||||
 Db 68292 GGAACAGACGACCTGGATCCAGAACAGAGGTCCTCCAGAGTTGGTACAGGCCAATTCCA 68351
 OY 495 SerHisMetProSerLeuHisAsnIleProValProGluTrpAsnTrpLeuGlyAsnThr 514
 |||||
 Db 68352 AGTCATATGCTTACTGCAATATATCCAGTCCGAGACCACTATCTAGGAAATACA 68411
 OY 515 ProThrMetProPheSerSerLeuProProTrpGluSerIleLeuTrpThrIleTrp 534
 |||||
 Db 68412 CCCACATGCACTCAGCTCTTCCACCAACAGAGTAA-----TGGGTCTTC 68459
 OY 535 AsnSer-ThrGlyIleGlnIleGlyAlaTrpAsnTrpMetGluIleGlyGlyThrSerSe 554
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 Db 68514 CTCTATTATTCAT 68526

KEYWORDS

HTG; HTGS_PHASE1.
 Rattus norvegicus.

SOURCE

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

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1 (bases 1 to 109832)
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Alsbrooks S.L., Amaralunge H.C., Are J.R., Ayale M., Banks T.,
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 Bouck J., Bowie S., Brieva M., Brown E., Brown M., Bryant N.P.,
 Bunay C., Burch P., Burkett C., Burrell K.L., Byrd N.C.,
 Carron T.F., Carter M., Cavazos S.R., Chacko J., Chavez D.,
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 Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R.,
 Davila M.L., Davis C., Davy-Carroll L., Dederich D.A.,
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 Hernandez O., Hodgson A., Hogues M., Hollway C., Hollins B.,
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 Jacobson B., Jia Y., Johnson R., Jolivet S., Joudah S.,
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 Lozado R.J., Lu X., Lucier A., Lucier R., Luna R., Ma J.,
 Maheshwari M., Mapua P., Martin R., Martindale A., Martinez E.,
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 Moser M., Neal D., Newton J., Newton N., Nguyen A., Nguyen N.,
 Nguyen N., Nickerson E., Nwokwuo S., Ogulu M., Okwundu G.,
 Oregana N., Oviedo R., Pace A., Payton B., Peary J., Perez L.,
 Petersen L., Pickens R., Primus E., Pu L.L., Quiles M., Ren Y.,
 Rives M., Rojas A., Rojibokan I., Rolfe M., Ruiz S., Savery G.,
 Scherer S., Scott G., Shen H., Shooshari N., Sison I.,
 Sodergren E., Sonalke T., Sparks A., Stanley H., Stone H.,
 Sutton A., Svatek A., Tabor P., Tamerisa A., Tamerisa K., Tang H.,
 Tansey J., Taylor C., Taylor T., Telford B., Thomas N., Thomas S.,
 Usmani K., Vasquez L., Vera V., Villalon D., Vinson R., Wang O.,
 Wang S., Ward-Moore S., Warren R., Washington C., Watlington S.,
 Williams G., Williamson A., Wleczyk R., Wooden S., Worley K.,
 Wu C., Wu Y., Wu Y.F., Zhou D., Zorrilla S., Nelson D.,
 Weinstock G. and Gibbs R.
 Title
 JOURNAL
 Unpublished
 2 (bases 1 to 109832)
 Title
 JOURNAL
 Unpublished
 3 (bases 1 to 109832)
 Title
 JOURNAL
 Submitted (23-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 18, 2002 this sequence version replaced gi:21039617.

COMMENT

Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information -----
 Center project name: GXXK
 Center clone name: CH230-515P13
 ----- Summary Statistics -----
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads

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Assembly program: Phrap: version 0.990329
Consensus quality: 64152 bases at least Q40
Consensus quality: 68753 bases at least Q30
Consensus quality: 71271 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hqsc.bcm.tmc.edu/docs/Cenbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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10626 10725: gap of unknown length
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* 79468 79568: gap of unknown length
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* /db_xref="taxon:10116"
* /clone="CH230-515P13"
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Score: 583.50 Matches: 115
Percent Similarity: 71.05% Conservative: 20
Best Local Similarity: 60.53% Mismatches: 48
Query Match: 16.46% Indels: 7
DB: 2 Gaps: 1
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OY 335 SerIaIhTgIuGInPrOgIySerIeuhIIsSerSergIuGlyMetGlyProVal 354
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OY 355 GluIuSerTTPpPeAlaProSerLeuGluHISProGInguIuAnGIuProSerLeu 374
Db 108118 GAGAGTCTGTTCTTCTCTCCCAAGAGACCAAGAGGAAGGAATGAGCCAGTGTG 108059
OY 375 GluIeSerLeuGInaSPGluAlaAsnTyHISLeuTySeraTgMetAspArgIn 394
Db 108058 CAGGCTAACGACGCAAGAGGAAGCCAGCTATCATCTTTTGGAAATATTGGGAAAAACAG 107999
OY 395 ThrIySGInGInPrOaTgGInAsnValAlaTyTAsnArgIuGInguIuArgATgArg 414
Db 107998 ACAAAATCACAGACCAAGCAATGAGGCTTACCAACAGAGAGCAAGCAAGCAAGC 107939
OY 415 ValSerHISaSPpPeAlaGInGInArgProTyGInuSnPheGInAsnThrGluGly 434
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OY 455 LeuThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPhe 474
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OY 495 SerHisMetProSerLeuHisAsnIleProValProGlyThrAsnTyrLeuGlyAsnThr 514
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***, 75 unordered pieces.
AC1311143
AC1311143.1 GI:22296630
VERSION
KEYWORDS
SOURCE
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Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 150691)
Muzny,D.,Marie., Metzker,M.,Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Ayalabebechi,V., Ayagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
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Cardenas,V., Carter,K., Cavazos,I., Cessari,H., Center,A.,
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Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,T., Garza,M.,
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Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hayes,A., Henderson,N., Hernandez,J.,
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Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
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Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorenzowa,L., Louisedge,H., Lozada,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,
Svatek,A., Tabors,T., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
Tingey,A., Trejos,Z., Usmari,K., Valas,R., Vera,V., Villaseca,D.,
Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R.,
Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
Holt,R.A., Smith,H.O., Weinstein,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 150691)
Rat Genome Sequencing Consortium.
Submitted (17-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GNUV
Center code name: CH230-76E20
----- Summary Statistics
Sequencing vector: plasmid;
Chemistry: Dye-terminator Big Dye 1008 of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 81272 bases at least Q40
Consensus quality: 88571 bases at least Q30
Consensus quality: 93815 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1
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* 48868 50740: contig of 1873 bp in length
* 50741 50840: gap of unknown length
* 50841 51862: contig of 1022 bp in length
* 51863 51962: gap of unknown length
* 51963 53332: contig of 1270 bp in length
* 53333 53332: gap of unknown length
* 53333 54925: contig of 1593 bp in length
* 54926 55025: gap of unknown length
* 55026 56755: contig of 1730 bp in length
* 56756 56855: gap of unknown length
* 56856 57957: contig of 1101 bp in length
* 57957 58056: gap of unknown length
* 58057 59061: contig of 1005 bp in length
* 59062 59161: gap of unknown length
* 59162 61652: contig of 2491 bp in length
* 61653 61752: gap of unknown length
* 61753 63890: contig of 2138 bp in length
* 63891 63990: gap of unknown length
* 63991 63991: gap of unknown length
* 63991 65953: contig of 1963 bp in length
* 65954 66053: gap of unknown length
* 66054 67490: contig of 1437 bp in length
* 67491 67590: gap of unknown length
* 67591 69106: contig of 1516 bp in length
* 69107 69206: gap of unknown length
* 69207 71641: contig of 2435 bp in length
* 71642 72997: contig of 1256 bp in length
* 72998 73098: gap of unknown length
* 73099 74227: contig of 1130 bp in length
* 74228 74327: gap of unknown length
* 74328 76444: contig of 2117 bp in length
* 76445 76544: gap of unknown length
* 76545 77677: contig of 1133 bp in length
* 77678 77777: gap of unknown length
* 77778 79397: contig of 1620 bp in length
* 79398 79497: gap of unknown length
* 79498 81346: contig of 1849 bp in length

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```

* 81347 81446: gap of unknown length
* 81447 83378: contig of 1932 bp in length
* 83379 83478: gap of unknown length

Alignment Scores:
Pred. No.: 2,29e-28 Length: 150691
Score: 583.50 Matches: 115
Percent Similarity: 71.05% Conservative: 20
Best Local Similarity: 60.53% Mismatches: 48
Query Match: 16,46% Indels: 7
DB: 2 Gaps: 1

US-09-981-397A-16 (1-671) x AC131143 (1-150691)

QY 335 SerAlaThrGluGlnProGlySerLeuHisSerSerGlnGlyMetCysProVal 354
   |||||
DB 113822 TCTGCTACAGAACCCGCTTCCGTCACAGTCCACAGGACTCCCATGGGACCTGTG 113763
   |||||

QY 355 GluGlnSerTrpPheAlaProSerLeuHisSerProGlnGluGlnGluProSerLeu 374
   |||||
DB 113762 GAGGAGTCTGCTTTCTTCTCCCTCCACAGTACCCACAGAGAACATGAGCGCAGTGTG 113703
   |||||

QY 375 GlnSerLysLeuGlnAspGlnAlaAsnTyHisLeuTyGlySerArgMetAspArgGln 394
   |||||
DB 113702 CAGGCTAAACCTCAGAGAGAACCCAGTATCATGCTTTGGCAATATTGCGGAAAAACAG 113643
   |||||

QY 395 ThrLysGlnGlnProArgGlnAsnValAlaTyAsnArgGluGlnGluArgArgArg 414
   |||||
DB 113642 ACAAATACACAGCCAGCGTGAATGAGCTTACACAGAGAGAGAAAGCAAGCAAGG 113583
   |||||

QY 415 ValSerHisAspProPheAlaGlnGlnArgProTyGluAsnPhGlnAsnThrGluGly 434
   |||||
DB 113582 GCTCCCATGACCCCTTTGCAAGCAGAGAGTCTATGAGAACTTAAGTCAAGTCCAGAGCA 113523
   |||||

QY 435 LysGlyThrValTySerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGly 454
   |||||
DB 113522 AAAGCTCTCTTATCCACACACCAACCATGGAATGCAAGCCACCGCTCTCAGCG 113463
   |||||

QY 455 LeuThrSerGlnProGlnValLeuTyGlnAsnAsnGlyLeuTySerSerHisGlyPhe 474
   |||||
DB 113462 CCAGCCAGCCAAATGAAGTCCACTTTGGACAGAGGATATATATCATCATCATGGGTTT 113403
   |||||

QY 475 GlyThrArgProLeuAspProGlyThrAlaGlyProAlaGlyValTrpTyArgProIlePro 494
   |||||
DB 113402 -----GGAGCTACAGGTACAGAGGTTGGTATGAGGCCAGGTGA 113364
   |||||

QY 495 SerHisMetProSerLeuHisAsnIleProValProGluThrAsnTyLeuGlyAsnThr 514
   |||||
DB 113363 AGCCCAATCATATATATAGCTTATATAACTCCAGTCCGCTGAGACCACTACAGAGACATTA 113304
   |||||

QY 515 ProThrMetProPheSerSerLeuProPro 524
   |||||
DB 113303 CCCACCATGCCATCATCTCTTGGCACCA 113274
   |||||

RESULT 14
ARI05327 1873 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 1 from patent US 6096539.
DEFINITION ARI05327
ACCESSION ARI05327
VERSION ARI05327.1 GI:12818924
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1873)
AUTHORS
Gomes,B,Charles., Kasof,G.M. and Prosser,J.Caroline.
TITLE
Protein activator of apoptosis
JOURNAL
Patent: US 6096539-A 1 01-AUG-2000;
FEATURES
Location/Qualifiers
source
1..1873
BASE COUNT 471 a 531 c 518 g 353 t
ORIGIN

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Alignment Scores:

Pred. No.: 1,24e-21 Length: 1873
Score: 448.00 Matches: 153
Percent Similarity: 42.52% Conservative: 100
Best Local Similarity: 25.71% Mismatches: 187
Query Match: 12.64% Indels: 156
DB: 6 Gaps: 22

us-09-981-397a-16 (1-671) x ARI05327 (1-1873)

1 MetInProAspMetSerLeuAsnValIleLys 117
147 CTGCACCTTCCTCAGCCTGATGCTGCTCAAGTTATGCCCCAGCGGTGCCCCCCCCC
12 MetLysSerSerAspPheLeuGluSerAlaGluLeu---AspSerGlyGlyPheGluLys 30
207 TTGGTGTTCATCGAAGAACTGGAGAACCGAGAGCTGCGGCAAGGCGGTTCGGCACA 266
31 ValSerLeuGlyPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGly 50
267 GTGTTCCGGGGCAACATAGAGAGTGGGCGC-----TACGATGTG 305
51 ProAsnGlyIleGluHisAsnGluAlaLeuLeuGluGluAlaLysMetMetAsnArgLeu 70
306 GCGGTCAAGATCGTAAGACTCGAAGCGCATATCCAGGGAGGTCAAGGCATGCAAGTCTG 365
71 ArgHisSerArgValIleLysLeuGlyValIleIleGluGluGly----- 86
366 GATACGCAATTCGTCGCTGCGCTGAGAAAGGGTATTCGAAAGGTGCGGCTCGAGCCAA 425
87 -----LysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeu 104
426 GATCCCAAGCGCGCTGTGCTGACTAATTCATGAGAGCGGCTCTTTCGGGCGTGTG 485
105 LysAlaGluMetSerThrProLeuSerValLysGlyArgIleLeuGluIleLeu 124
486 CAGTCCCAAGTCCCTGCGCCCTGCGCTCTTTCGCTGCTGAAAGAGTGTGCTT 545
125 GlyMetCysTyrLeuHisGlyLysGly-----ValIleHisLysAspLeuLysPro 142
546 GGGATGTTTACCTGCGACGACGACCAACCGGCTGCTGCGACCGGAGCTTCAAGCCATCC 605
143 AsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPhe 162
606 AACCTCTGCTGAGCCAGACGCTGACGCTCAAGTGGCAGATTTGGCTGTGCCCATTT 665
163 LysMetIrrPserLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAspLysThr 182
666 CAGGAGGCTTCACAG-----TCAGGGACA 689
183 AlaLys---LysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspAla 201
690 GGGTCCCGGAGACGAGGAGGACCTGGCTGCTGCTGCGACCAAGCTGTTGTTACCTA 749
202 AsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValAlaLeuTyrPalaIle 221
750 AACCGGAGGCGCTCCACAGCAGTGTACAGCTTCGGGATTCCTAATGTGGCAGTGTG 809
222 PheAlaAsnLysGlu-----ProTyrGlu-----AsnAlaIleCys 233
810 CTTCCTGGAAGAGAGTTGAGTTGCCAACCACCATCCTGCTAGCAGACAGTGTGC 869
234 GluGlnGluLeuIleMetCysIleLysSerGlyAsnThrProAspValAspAspLeuThr 253
870 AACGAGGAG-----AACCGGCTTCATTTGGCTGAGTGTGCC 905
254 GluTyrCysProArgGlu-----IleIleSerLeuMetLysLeuCysTyr 268
906 CAAGCGGCGCTGAGACTCCCGGCTTAGAAGAGCTGAAGAGAGCTATACACTCTGCTGCG 965
269 GluAlaAsnProGluAlaArgProThrPhe-----ProGlyIleGluGluLys 284

966 AGCAGTGAAGCCCAAGACAGACCTCTTCAGGAATGCTTACCAAAACTGATGAGTTC 1025
285 PheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspValLysSerLeu 304
1026 TTCCAG-----ATGTTGGAGAACATATGATGCTGCTGTCCACAGGTA 1070
305 LysLysGluTyrSerAsnGluAsnAlaValAlaValLysArgMetGlnSerLeuGlnAsp 324
1071 AAGGATTTCTGCTCTCAGCTCAGACGACGACCATAGAGATT----- 1112
325 CysValAlaValProSerSerArgSerAsnSerAlaThrGlnGluProGlySerLeuHis 344
1113 -----TCTATCCAGAGTCA----- 1127
345 SerSerGlnGlyLeuGlyMetGlyProValGluGluGluSerThrPheAlaProSerLeuGlu 364
1128 -----GGCCAAAGAGAGGACAGAAATGATGCTTTAGAGAAACCATAGAA 1172
365 HisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGluAspGluAsnTyr 384
1173 AACGACACTCTCTGATGATGCTCATGTTTGTGAGTGGTA----- 1214
385 HisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAla 404
1215 -----AACAACTGAATTAAGAGAGCTCCAGCTCTGTT--- 1250
405 TyrAsnArgGluGluGluArgArgArgValSerHisAspProPheAlaGlnIleArg 424
1251 -----CCTAA-AAATGCCCGAG 1267
425 ProTyrGluAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSer-SerAlaLase 444
1268 CCTTACCAAGAGAGACAGGAGGACAGAGAGAGAGTTCACAGAGCTGACAGCAGGAC 1327
444 HisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrG1 464
1328 ATCTTCAGATTCGATGAGGCCCAACT-----CCCGAGACTCCAGAGCTCAACTTT 1378
464 AsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyTyrAla 484
1379 CAGAAACAGATGCCACG-----CCTACCTCAACTGAGAACAA-- 1415
484 aglyProArgValIrrTyrArgProIleProSerHisMetProSerLeuHisAlaLeu 504
1416 -----CCAAAT-----CC 1423
504 ovalProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuPro 524
1424 TGGACCCCGAGGAAATCAGGGGCTGAGAGACAAAGCATGTGCTCGAGAGACCC 1483
524 cThrAspGluSerIleLys-----TyrThrIleTyrAsnSerThrGlyTleG1 540
1484 GGAGCCAAATCCAGTAAACAGGAGGCGACCGCTGTTAACTATTAACAATCTCTTGGGGTCA 1543
540 nileGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSer 554
1544 AGTTGGAGACAAACAACACTTGTGACTATGACATGACACAGCACTGCTC 1586

RESULT 15
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LOCUS Sequence 1 from Patent WO0077200.
DEFINITION AX067676
ACCESSION AX067676
VERSION AX067676.1 GI:12329570
KEYWORDS
SOURCE human:
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1873)
AUTHORS Gomes,B.C., Kasol,G.M. and Prosser,J.C.
TITLE Receptor interacting protein rip3
JOURNAL Patent: WO 0077200-A 1 21-DEC-2000;

Astrazeneca AB (SE)
Location/Qualifiers
1. 1873
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 471 a 531 c 518 g 353 t
ORIGIN

Alignment Scores:
Pred. No.: 1.24e-21 Length: 1873
Score: 448.00 Matches: 153
Percent Similarity: 42.52% Conservative: 100
Best Local Similarity: 25.71% Mismatches: 187
Query Match: 12.64% Indels: 156
Gaps: 22

US-09-981-397a-16 (1-671) x AX067676 (1-1873)

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OY 1 MetGlnProAspMetSerLeuAsnValIleLys----- 11
DB 147 CTGGCACCCTTCAGCCCTGATGCTGCTCAAGTATGAGCCAGCGGTGCCCCCCCCC 206
OY 12 MetLysSerSerAspPheLeuGluSerAlaGluLeu---AspSerGlyGlyPheGlyLys 30
DB 207 TTGGTGTCCATCGAGAACTGGAGAACCCAGAGCTCGGCCAAAGGGGTTCGGCACA 266
OY 31 ValSerLeuGlyPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGly 50
DB 267 GTGTTCCGGGGGCAACATAGGAGAGGGGC-----TACATGTG 305
OY 51 ProAsnGlyIleGlnHisAsnGluAlaLeuGluGluAlaLysMetMetAsnArgLeu 70
DB 306 GCGGTCAAGATCGTAACTCGAAGCGGATATCCAGAGGAGTCAGAACGCCATGCGACGTG 365
OY 71 ArgHisSerArgValValLysLeuGluGlyValIleGluGluGly----- 86
DB 366 GATACGAAATTCGCTGCGCTGAGAGGGGTATCGAAGGCTGCGGCGCTCGAGCCA 425
OY 87 -----LysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeu 104
DB 426 GATCCCAAGCGCGCTGCTGCTGACTAATTCAATGGAGAACGGCTCTTTCGGGGCTGCTG 485
OY 105 LysAlaGluMetSerThrProLeuSerValLysGlyArgGlyIleLeuGluIleGlu 124
DB 486 CAGTCCCAAGTCCCTCGGCGCTGCGCTTTCCTTCCGCTTAAAGAAAGTGTGCTT 545
OY 125 GlyMetCysTyrLeuHisGlyLysGly-----ValIleHisLysAspLeuLysProGlu 142
DB 546 GGGATGTTTACCTGACGACGACCAACCGGCTGCTCGACCGGGACCTCAAGCCATCC 605
OY 143 AsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPhe 162
DB 606 AACGTCCTGCTGAGCCAGAGCTGCAAGCTCAAGTATTTGGCTGTCCACATTT 665
OY 163 LysMetTrpSerLysLeuAsnAsnGluGlnHisAsnGluLeuArgGluValAspGlyThr 182
DB 666 CAGGAGGCTCAGAG-----TCAGGAGACA 689
OY 183 AlaLys---LysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspVal 201
DB 690 GGGTCCGGGGAGCCAGGGGGACCTGGGCTACTGGCCCAAGACTGTGTTTAAGCTA 749
OY 202 AsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValValLeuTrpAlaIle 221
DB 750 AACCGAAGGGCTCCACAGCCAGTGTACACTTCGGGATTCCTAATGTGGGCACTG 809
OY 222 PheAlaAsnLysGlu-----ProTyrGlu-----AsnAlaIleCys 233
DB 810 CTTCCTGGAGAGAGAGTGTAGTTGCAACGAAACATCATCTGCTACGAGCAAGTGTGC 869
OY 234 GluGlnGlnLeuIleMetCysIleLysSerGlyAsnArgProAspValAspAspIleThr 253
DB 870 AACAGGCGAG-----AACCGGCTTCATTTGGCTGAGCTGCC 905

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OY 254 GluTyrCysProArgGlu-----IleIleSerLeuMetLysLeuGlyTrp 268
DB 906 CAGCGCGGGCTGAGACTCCCGGCTTAGAAGGACTGAAGAGACTTATGACAGCTTCTGCG 965
OY 269 GluAlaAsnProGluAlaArgProThrPhe-----ProGlyIleGluGluLys 284
DB 966 AGCACTGAGGCCAGAGACACCTTCCTTCAGGAATGCTTCACAAAATGATGATGATC 1025
OY 285 PheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspValLysSerLeu 304
DB 1026 TTCGAG-----ATGGTGGAGAACATATGATGCTGCTCTCCACGGTGA 1070
OY 305 LysLysGluTyrSerAsnGluAsnAlaValValLysArgMetGluSerLeuGlnLeuAsp 324
DB 1071 AAGGATTCCTCTCTCAGCTCAGGAGCCAAATAGACATTT----- 1112
OY 325 CysValAlaValProSerSerArgSerAsnSerAlaThrGlnGluProGlySerLeuHis 344
DB 1113 -----TCTATCCAGACTCA----- 1127
OY 345 SerSerGlnGlyLeuGlyMetGlyProValGluGluSerTyrPheAlaProSerLeuGlu 364
DB 1128 -----GGCCAAAGAGGAGCAGACAAATGATGCTTTAGGAGAACCATAGAA 1172
OY 365 HisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyr 384
DB 1173 AACCAAGCACTCTGTAATGATGCTATGCTTCTGAGTGCCTA----- 1214
OY 385 HisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAla 404
DB 1215 -----AACAACTGATCTAGAGGAGCCCTCCAGCTGTCT--- 1250
OY 405 TyrAsnArgGluGluGluAlaArgArgArgValSerHisAspProPheAlaGlnIleArg 424
DB 1251 -----CTTAA-AAATGCCCGAG 1267
OY 425 ProTyrGluAsnPheGlnAsnThrGlnGluLysGlyThrValTyrSer-SerAlaAlaSer 444
DB 1268 CCTTACCAAGAGGAGACAGGCGCCAGAGAGAGAGTTCACAGCTGAGCAGCGGAC 1327
OY 444 HisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlu 464
DB 1328 ATCTTCAGATTCGATGGCCCAACCT-----CCCAAGACTCCAGAGACCTCACTTT 1378
OY 464 AsnAsnGlnLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAl 484
DB 1379 CAGAAACCAAGATGCCAGC-----CCTTACCTCAACTGAGACA-- 1415
OY 484 ArgLysProArgValTyrTyrArgProIleProSerHisMetProSerLeuHisAsnIlePr 504
DB 1416 -----CCAAAT-----CC 1423
OY 504 OValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuProTr 524
DB 1424 TGGACCCCGAGGAGATCGAGGGCTGAGAGACAAAGCATGAATGCTGCTCAGAGCAACC 1483
OY 524 CThrAspGluSerIleLys-----TyrThrIleTyrAsnSerThrGlnGlyIleGlu 540
DB 1484 GGAGCCAAATCCAGTAACAGGAGCGGCTGTTAACATATATACACTCTCTGGGGGTGA 1543
OY 540 nIleGlyAlaTyrAsnTyrMetGluIleGlyGlyTyrHisSerSer 554
DB 1544 AGTTGGAGACAAACACTACTTGTACATATGCAACAGCAACTGCTGC 1586

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Search completed: June 25, 2003, 21:58:59
Job time : 4230 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2003, 19:48:48 ; Search time 371 Seconds
(Without alignments)
4073.021 Million cell updates/sec

Title: US-09-981-397A-16
Perfect score: 3545
Sequence: 1 MOPDMSLWIKMKSSDFLES.....ALHCCSRIDLSSLIYVSQN 671

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=N-Geneseq.101002 -QWTF=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Database : N-Geneseq.101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3545	100.0	2016	22	AAF86480
2	3545	100.0	2016	23	AA880489
3	3545	100.0	2617	21	AA289748
4	3545	100.0	2617	24	ABN81397
5	3545	100.0	2617	24	ABN81170
6	3539	99.8	2016	18	AAT66408
7	3513	99.1	2137	18	AAT43753
8	3505	98.9	9687	22	AA538810
9	3505	98.9	9687	22	ABK15129
10	2899	81.8	3750	20	AAV99818
11	2423.5	68.4	2268	18	AAT43752
12	2423.5	68.4	2268	20	AAV99827
13	1531	43.2	2879	23	AA580491
14	521	14.7	606	22	AA280411
15	461.5	13.0	1871	22	AAK94599
16	448	12.6	1873	21	AAA47701
17	448	12.6	1873	22	AAD16312
18	446	12.6	1557	21	AAA47702
19	446	12.6	1557	22	AAD16313
20	441.5	12.5	2140	21	AA475675
21	440.5	12.4	1887	23	ABK43722
22	440	12.4	1697	22	AAE28898
23	435	12.3	1557	21	AA250788
24	423.5	11.9	3876	22	AAH15762
25	410.5	11.6	2370	21	AA261161
26	410.5	11.6	3516	21	AA261784
27	410.5	11.6	3516	22	AA299717
28	410.5	11.6	3516	22	ABL34869
29	409.5	11.6	1700	24	ABL34883
30	408.5	11.5	1774	21	AAZ61830
31	408.5	11.5	1774	22	AAZ61830
32	408.5	11.5	1774	24	ABL34915
33	408.5	11.5	2015	24	ABK62584
34	408.5	11.5	2294	21	AA258584
35	405.5	11.4	1437	22	AAE30546
36	403.5	11.4	2355	24	ABA90356
37	397.5	11.2	2499	22	AA506739
38	377	10.6	366	21	AA503316
39	375.5	10.6	1888	21	AA261671
40	375.5	10.6	1888	22	AAC99604
41	375.5	10.6	1888	24	ABL34756
42	371	10.5	1619	24	AA40753
43	371	10.5	1931	20	AA209246
44	371	10.5	1931	22	AAE30001
45	371	10.5	1931	24	AA40752

ALIGNMENTS

RESULT 1
ID AAF86480 standard: cDNA: 2016 BP.

AC AAF86480;
XX 28-JUN-2001 (first entry)

DE Human Receptor Interacting Protein, hRIP, coding sequence.

XX Human: Receptor Interacting Protein; hRIP; antibacterial; cytostatic;
antiflammatory; gene therapy; infection; genetic disease; neoplasia;

KW Tumour necrosis factor Receptor Associated Factor-2; TRAF2; TRADD;

KW Tumour necrosis factor Receptor Associated Death Domain protein;

KW Inflammation; hypersensitivity; ss.

OS Homo sapiens.

XX

Key Location/Qualifiers
 1..2016
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 /product="Human RIP"

US6211337-B1.

03-APR-2001.

11-AUG-1998; 98US-0132118.

23-OCT-1995; 95US-0553727.

(TULA-) TULARIK INC.

Batchwal VR, Huang J, Hsu H, Goeddel DV;
 WPI: 2001-334617/35.
 P-PSDB; AAB82091.

New receptor interacting protein polypeptide having threonine in position 514 useful in screening assays for agents that modulate interaction of protein with its binding targets

Disclosure: Columns 7-12; 10pp; English.

The present sequence is the coding sequence for human Receptor Interacting Protein (RIP). RIP is useful in screening assays for agents that modulate the interaction of RIP with its natural binding targets, especially substrates such as Tumour necrosis factor Receptor Associated Factor-2 (TRAF2) and Tumour necrosis factor Receptor Associated Death Domain protein (TRADD). The agents are potentially useful for the treatment and diagnosis of diseases, e.g. infections, genetic diseases, neoplasia, inflammation and hypersensitivity.

Sequence 2016 BP; 629 A; 446 C; 514 G; 427 T; 0 other:

Alignment Scores:
 Pred. No.: 4.2e-264 Length: 2016
 Score: 3545.00 Matches: 671
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-981-397a-16 (1-671) x AAF6480 (1-2016)

QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
 |||||||
 Db 1 ATGCAGACGACAGATGCTCTTAATGTCATTAAGATGAATCCAGTGCCTCGAGAGT 60

QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisArgThrGlnGly 40
 |||||||
 Db 61 GCAGACACGACGACGAGGAGGCTTGGAGAGGTGCTCTGCTTTTCCACAGACCCAGGGA 120

QY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnGlyIleGluHisAsnGluAlaLeu 60
 |||||||
 Db 121 CTCATGATCATGATAAAGAGTGTACAAAGGGGCCCAACTCATTTGACACAGAGAGCCCTC 180

QY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGly 80
 |||||||
 Db 181 TTGGAGGAGGCGAAGATGATGACAGACTGACACACACCGGCTGCTAAAGCTCTCGGC 240

QY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
 |||||||
 Db 241 GTCATCATAGAGAGAGGAAGTACTCCCTGGTATGAGTACATGAGAGAGGCAACTG 300

QY 101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
 |||||||
 Db 301 ATGACAGGTCTGAAGCCGAGATGATGCTCCGCTTCTGTAAAGAGAGATATTTTG 360

QY 121 GluIleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
 |||||||

Db 361 GAAATCATTTGAAGCAATGCTACTTACATGAGAAAAGGCGTGTATCCACAGAGCACTGAAG 420

QY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
 |||||||

Db 421 CCTGAATATCTCTGTGATATATGACTTCCACATTAAGATGCGAGACCTGGCCCTTCC 480

QY 161 SerPheLysMetIlePheSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp 180
 |||||||

Db 481 TCCTTTAAGATGTGAGGACCAACTGATATATGAGAGCAACATGAGCTGAGGAGAGTGCAC 540

QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAsp 200
 |||||||

Db 541 GGCACGCTTAAGAAAGAAATGGCGGACCCCTACTACTCATGAGGCGCCGACCACTGAATAC 600

QY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuThrAla 220
 |||||||

Db 601 GTCAAGCAAAAGCCACAGAGAAAGTGGATGTACACCTTGGCTGTGTCTCGGGCG 660

QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGluLeuIleMetCys 240
 |||||||

Db 661 ATATTGCAATTAAGGACCCATATCAAAATGCTATCTGTGACGACAGTGTATATATGTC 720

QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
 |||||||

Db 721 ATAAATCTGGGAAAGCGCCAGATGTGATGATCATCTACTGATCTCCCAAGAGAAAT 780

QY 261 IleSerLeuMetLysLeuGlySerProGluAlaAsnProGluAlaArgProThrPheProGly 280
 |||||||

Db 781 ATCAGCTCATAGACCTCTGCTGGAGACCAATCCGAAAGCTGGCGGACATTTCTCTGCG 840

QY 281 IleGluGluLysPheArgProPheTyrLeuSerGluGluGluGlyLeuValGluLysAsp 300
 |||||||

Db 841 ATTGAGAGAAATTTAGGCGCTTTTATTTAAGTCAATTAAGAAAGAGTGAAGAGAGAC 900

QY 301 ValLysSerLeuLysLysGlyLysTyrSerAsnGluAsnAlaValValLysArgMetGlnSer 320
 |||||||

Db 901 GTGAAGAGCTTTAAAGAAAGATATTCAAACGAAATGCAGTGTGAGAAATGACAGTCT 960

QY 321 LeuGluIleuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
 |||||||

Db 961 CTTCACCTGATGTGTGGCAGTACTTCAAGCCGGTCAAAATTCAGCCACAGAAACAGCT 1020

QY 341 GlySerLeuHisSerSerGluGlyLeuGlyMetGlyProValGluGluSerThrPheAla 360
 |||||||

Db 1021 GGTTCACGTGACAGTTCCTCCAGGAGTGTGGATGGTCTCTGTGGAGAGATCTCGTTTCT 1080

QY 361 ProSerLeuGluHisProGluGluGluAsnGluProSerLeuGlnSerLysLeuGlnAsp 380
 |||||||

Db 1081 CTTTCCCTGGAGCCACCCACAGAAAGAGATGAGCCACCTGCAGAGTAACTCCAAAGAC 1140

QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGluGlnProArg 400
 |||||||

Db 1141 GAGGCAACTACCATCTTTATATGCGAGCCGATGACAGAGCGACAGCAACAGCAGCCGAGA 1200

QY 401 GlnAsnValAlaTyrAsnArgGluGluGluAlaArgArgArgValSerHisAspProPhe 420
 |||||||

Db 1201 CAGATGTGGCTTACACAGAGAGAGGAAAGAACACAGGAGTCCCATGACCTTTT 1260

QY 421 AlaGluGlnArgProTyrGluAsnPheGluAsnThrGluGlyLysGlyThrValTyrSer 440
 |||||||

Db 1261 GCACAGCAAAAGACCTTTACAGAAATTTTACAGATACAGAGGAGGAGGACATGTTATTC 1320

QY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGluProGln 460
 |||||||

Db 1321 AGTGAGGCAAGTATGATATGCACTGACACCAAGCTTATGAGGCTTACCAAGCAACTTAA 1380

QY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
 |||||||

Db 1381 GTACTGATACAGAAACATGATATATATGCTACATGCTTTGGAAACAGCACTGAT 1440

QY 481 ProGlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeu 500
 |||||||

Db 1441 CCAGGACAGCAGGTCGCCAGAGTTGTGTACAGGCCAATTCCAAGTCATATCTCTAGTCTG 1500

OY	501	HisasnIleProValProGluThrAsnTyrIleuGlyAsnThrProHmeProPheSer	520
Db	1501	CATATATCCACGAGTCCCTGAGACCACTATCTAGGAATTAACCCACCATTCATTCAGC	15606
OY	521	SerLeuProProThrAspGluSerIleIleuSTyThrIleTyrAsnSerThrGlyIle61n	540
Db	1561	TGCTTGGCCACCAAGATGAACTATATAAATATACATATACATATAGTACGATTCAG	16206
OY	541	IleGlyAlaTyrAsnTyrMetGluIleGlyIlyThrSerSerSerLeuAspSerThr	560
Db	1621	ATTTGAGCGCTCAATTTATATGAGATTGTGGACGAGTTCATCATCTAGACAGACA	16806
OY	561	AsnThrAsnPhelySGluGluProAlaIalAsyTyrGlnIalIlePheAspAsnThrThr	580
Db	1681	AATACGAACCTTCAAGAGAGACCGACGCTGATGATTCACAGCTATCTTGATAAATCACT	17406
OY	581	SerLeuThrAspLysHisIleuAspProIleArgGluAsnLeuGlyLysHisTSPlysAsn	600
Db	1741	AGTCTGACGCGATTAACACCTGACCCCATATCAGGAAATCTGGGAAAGCACTGGAAAAAC	18006
OY	601	CysAlaIarGlySleuGlyPheThrGlnSerGlnIleAspGluIleAspHisAsPTyGlu	620
Db	1801	TGTCCCGCGTAAACGTGGGCTTCACACAGTCTCAGATTGATGAATTGACCAATGACTATCAG	18606
OY	621	ArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTSPValMetArgGluGly	640
Db	1861	CGAGATGACCTGGAAGAAAGAAAGCTTTACCAAGATGCTCCAAAGTGGGTGATAGGGAAGGC	19206
OY	641	IleLysGlyAlaThrValGlyLysLeuAlaGlnIalLeuHisGlnCysSerArgIleAsp	660
Db	1921	ATTAAGGAGGACGAGGTGGGGAACCTGGCCAGCGCGTCCACAGTGTTCAGAGATCGAC	19806
OY	661	LeuLeuSerSerLeuIleTyrValSerGlnAsn	671
Db	1981	CTTCTGAGCAGCTTGATTACGTACGCCAGAAC	2013
RESULT 2			
ID	AAS80489	standard; cDNA; 2016 BP.	
AC	AAS80489;		
XX	13-FEB-2002 (first entry)		
DE	DNA encoding novel human diagnostic protein #16293.		
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KW	Food supplement; medical imaging; diagnostic; genetic disorder; ss.		
XX	Homo sapiens.		
OS	WO200175067-A2.		
FN	11-OCT-2001.		
XX	30-MAR-2001; 2001WO-US08631.		
PE	31-MAR-2000; 2000US-0540217.		
PR	23-AUG-2000; 2000US-0649167.		
XX	(HYSE-) HYSEQ INC.		
PA	Drmanac RT, Liu C, Tang YT;		
XX	WT: 2001-639362/73.		
DR	P-PSDB; ABG16302.		
XX	New isolated polynucleotide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity -		
XX			

PS	Claim 1 SEQ ID No 16293; 103pp: English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAs64197-AAs94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/publ/published_pct_sequences .
CC	
XX	
SO	Sequence 2016 BP; 629 A; 446 C; 514 G; 427 T; 0 other.
	Alignment Scores:
	Pred. No.: 4.2e-264 Length: 2016
	Score: 3545.00 Matches: 671
	Percent Similarity: 100.00% Conservative: 0
	Best Local Similarity: 100.00% Mismatches: 0
	Query Match: 100.00% Indels: 0
	DB: 23 Gaps: 0
US-09-381-397A-16 (1-671) x AAS80489 (1-2016)	
QY	1 MetGlnProaspMetSerLeuAsnValIleuysMeLysSerSeraspPheLeuGluSer 20
Db	1 ATTCACAACCGACGATGCTCTTGAATGTCATTAAGATGAATCCACGTCTTCGGAAGT 60
QY	21 AlaGluLeuAspSerGlyValPheGlyLysValSerLeuGlyPheAspArgThrGlyGly 40
Db	61 GCAGACCTGGACGCGGAGGCTTTGGAAAGGTCTCTGTCTTCCACAGAACCCAGGGA 120
QY	41 LeuMetLleMeLysThrValTyrLysGlyProAsnGlyIleGluHisAsnGluAlaLeu 60
Db	121 CTCATGATCATGAAGAACGTCATCAACAGGGGCCCACTGATGACACACAGAGCCCTC 180
QY	61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuGly 80
Db	181 TTGGACGAGCGCAAGATGATGATGAACAGACTGAGACACACCCGGGTGGTGAAGCTCTGGGC 240
QY	81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
Db	241 GTGATCATGAGAGGAAGGAGTACCTCTGGTGAAGGAGTGCATGAGGAAAGGCAACCTG 300
QY	101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgGlyIleLeu 120
Db	301 ATGCACGCTCTGAAGCCGAGATGAGTACTCCGCTTCTGTAAGAAGAGAGATATTTTG 360
QY	121 GluIleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
Db	361 GAATCATTTGAAGGATGTGCTACTTACATGTAAGAAAGCGGTGATACCAAGAGACTGAAG 420
QY	141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleIleAspLeuGlyLeuAla 160
Db	421 CCGAAGAAATATCTTGTGATTAATGACTTCCACATTAAGATCCGAGACCTGGCGCTTGGC 480
QY	161 SerPheLysMetTyrSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp 180
Db	481 TCCCTTTAAGATGTGGAGCAACCTGATATATGAAGACCAATGAGCTGAGGGAAGTGGAC 540
QY	181 GlyThrAlaLysLysAsnGlyClyThrLeuTyrTyrMetAlaProGluHisLysAsnAsp 200

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|||||
541 GGCACCGCTAAGAAAGATGGCGGACCCCTACTACATGGCGCCGAGACCTGATGAC
Db
ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuThrPhe
OY 201
601 GTCAACGAAAGCCACAGAGAGTGGATGTGTACAGCTTGCTGTGTACTCTGGGGG
Db
221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGluLeuIleMetCys
OY 240
661 ATATTGGCAATTAAGAGCCATATGAATGTATCTGTGAGCAGAGTTGATATGTGC
Db
241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle
OY 260
721 ATAAATCTGGGAAGAGCCAGCATGTGATGATGATGATGATGATGATGATGATGAT
Db
261 IleSerLeuMetLysLeuCysTyrGluAlaAsnProGluAlaArgProThrPheProGly
OY 280
781 ATCACTCATGAGACCTCTGCTGGAGAGCAATCCGGAGAGCTGGCCGACATTTCTGGC
Db
281 IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluLysSerValGluLysAsp
OY 300
841 ATGAAGAAAATTTAGGCTTTTATTATTAAGTCAATTAGAGAAGTGTAGACAGAGC
Db
301 ValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValValLysArgMetGlnSer
OY 320
901 GTGAAGAGTTAAAGAAAGATATTCAAACGAAATGAGTGTGAGAGAAATGACAGTCT
Db
321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnGlnPro
OY 340
961 CTTCACTTGATTTGTGTGACACTACCTTCACCGGTCGTAATTCAGCCACACAGAGCTT
Db
341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTyrPheAla
OY 360
1021 GGTTCACTGACAGAGTCCAGAGACTGGGATGGTCCGTGGAGAGAGCTCGTTGTGT
Db
361 ProSerLeuGlnHisProGlnGluLysAsnGluProSerLeuGlnSerLysLeuGlnAsp
OY 380
1081 CTTTCCTGGAGACCCACAAAGAGATGAGCCAGCTGACAGATTAAGTCCACAGAC
Db
381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg
OY 400
1141 GAAGCACTACCATCTTTATGTGACCGCCGATGAGCAGGACAGACAGACAGCCCGACA
Db
401 GlnAsnValAlaTyrAsnArgGluGluLysArgArgArgValSerHisAspProPhe
OY 420
1201 CAGATGTGGCTTACACAGAGAGAGAAAGACAGAGAGCTCCCATGACCTTTT
Db
421 AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValLysSer
OY 440
1261 GCACAGCAAGACCTTACGAGATTTTCAGATACAGAGGAAAGGACAGCTTATTTCC
Db
441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln
OY 460
1321 AGTGAGCGCAGTACAGTATATGCACTGACACCGCCCTGAGGCTACACAGCACTTCA
Db
461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp
OY 480
1381 GTACTGTATCGAACAATGATATATATAGCTCATATGCTTGGAAACAGACCATGTGAT
Db
481 ProGlyThrAlaGlyProArgValThrPyrArgProIleProSerHisMetProSerLeu
OY 500
1441 CCAGAGACAGAGGCTCCAGAGTTGTGACAGGCCAATTCAGATATGCTGAGTGTG
Db
501 HisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSer
OY 520
1501 CATATATCCAGTCCCTGAGAGCACTATCTAGAAATACACCAATGCAATGCAATTCAC
Db
521 SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln
OY 540
1561 TCCCTGACCAACAGATGATCTTAAATATACCATATACAAATAGTACTGCAATCAG
Db
541 IleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerLeuLeuAspSerThr
OY 560
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Db 1621 ATTGAGCCCTACAAATTATATGAGATTTGTGGAGAGTTCATCAGTACTAGACAGACA
OY 561 AsnThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr
Db 1681 AATAGCACTTAAAGAAAGAGCCAGCTGTAAGTACCAAGCTATCTTGTATATATCCACT
OY 581 SerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisThrPlyAsn
Db 1741 ACTGTGACGATAAACACTGTGAGCAACATCAGGAAATCTGGAAAGACATGAGAAAC
OY 601 CysAlaAlaGlyLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGlu
Db 1801 TGTGCCCGTAACTCGGCTTACACAGTCTGATGATGATGATGATGATGATGATGATGAT
OY 621 ArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTyrValMetArgGluGly
Db 1861 CGAGATGAGCTAAAGAAAGTTTACAGATGCTCCAAAGTGGGTGATGAGGAGAGC
OY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp
Db 1921 ATAAAGGAGCCAGGTTGGGAGAGCTGGCCAGGCGCTCCACAGCTGTCCAGATCGAC
OY 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn
Db 1981 CTTCTGAGCAGCTGATTTACGTACGACAGAAC
OY 671

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RESULT 3

AA289748 standard, DNA; 2617 BP.

AA289748;

05-MAY-2000 (first entry)

Human RIP-1 nucleotide sequence.

RIP-1; RalBP; RLIP; antisense inhibitor; anti-inflammatory; cytostatic; anti-infective; diagnose; prevent; treatment; tumour formation; ds.

Homo sapiens.

US6020198-A.

01-FEB-2000.

25-SEP-1998; 98US-0161443.

25-SEP-1998; 98US-0161443.

(ISIS-) ISIS PHARM INC.

Bennett CF, Cowsest LM;

WPI: 2000-146889/13.

P-PSDB: AAT78502.

Antisense inhibition of human RIP-1 expression, useful for diagnosing, preventing and treating conditions such as inflammation -

Claim 1; Column 29-36; 26pp; English.

This sequence represents the human RIP-1 nucleotide sequence. RIP-1 (also known as RalBP1 and RLIP) is a GTPase activating protein (GAP) thought to be a downstream target of Ral. The invention relates to RIP-1 antisense phosphorothioate oligonucleotides with anti-infective, anti-inflammatory and cytostatic activity. The oligonucleotides are RIP-1 antisense inhibitors and are used in the diagnosis, prevention and treatment of conditions associated with RIP-1 expression. Conditions associated with RIP-1 expression include various infections, inflammation and tumour formation.

Sequence 2617 BP; 794 A; 586 C; 659 G; 574 T; 4 other;

Alignment Scores:

Prod. No.:	5.88e-264	Length:	2617
Score:	3545.00	Matches:	671
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-981-397a-16 (1-671) x AAZ89748 (1-2617)

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OY 1 MetClnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
Db 1 ATGCACACAGACAGTCTTGAATGATTAAGTGAATTCAGTGAATCTTCTCTGAGAGT 60
OY 21 AlaGlnLeuAspSerGlyGlyPheGlyLysValSerLeuGlnSerPheHisArgThrGlnGly 40
Db 61 GCAGAACTGGACAGCGAGGCTTTGGAGAGGTCTCTGTCTTTCCACAGAACCCAGGGA 120
OY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnGlnIleGlnHisAsnGlnValAlaLeu 60
Db 121 CTCATGATCATGAAGAACAGTGTACAGAGGCCCCAAATGCATTTGAGCACAGAGGCCCTC 180
OY 61 LeuGlnGlnAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuGlnGly 80
Db 181 TTGGAGAGGCGGAGATGATGAACAGACTGAGACACAGCCGGGTGTGAACCTCTGGGC 240
OY 81 ValIleIleGlnGlnGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
Db 241 GTCTCATATAGAGAGGAAAGTACTCCCTGGTGTGATGATGATGATGAGAGAGGCAACTG 300
OY 101 MetHisValLeuLysAlaGlnMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
Db 301 ATGCAGCTGGCGAAGCGAGATGAGTACTCCGCTTCTCTTAAGAGAGATATTTTG 360
OY 121 GlnIleIleGlnGlyMetCysTyrLeuHisGlnLysGlyValIleHisLysAspLeuLys 140
Db 361 GAAATTCATTGAAGAAATGCTTACTACTATGGAAGAGCGGATACAAAGACTGTGAG 420
OY 141 ProGlnAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
Db 421 CCTGAATAATCTCTTGTGATTAAGACTTCCACATTAAGATGCGAGACTTGGCCCTGGCC 480
OY 161 SerPheLysMetIlePheLysLeuAsnAsnGlnLysHisAsnGlnLeuArgGlnValAsp 180
Db 481 TCCTTTAAGATGTGAGCAAACTGATATGAAGACACATGAGCTGAGGAAAGTGGAC 540
OY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGlnHisLeuAsnAsp 200
Db 541 GGCACCCCTTAAGAAATGGCGGCCCTTACTACTACATGCGGCCGAGCACTGAATGAC 600
OY 201 ValAsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValIleuThrAla 220
Db 601 GTCAACCAAGGCCCAAGAGAGAGTGTGATGAGCTTGTGATGATCTCTGGGCG 660
OY 221 IlePheHisAsnLysGlnProTyrGlnAsnAlaIleCysGlnGlnGlnIleuIleMetCys 240
Db 661 ATATTTCGAATATAGAGCCATATGAATGCTATCTGTGAGCAGCAAGTTGATATGCGC 720
OY 241 IleLysSerGlnAsnArgProAspValAspAspIleThrGluTyrCysProArgGlnIle 260
Db 721 ATAAAACTCTGGAGACAGCCAGATGTGATGATCACTGACTGCTCCCAAGGAATTT 780
OY 261 IleSerLeuMetLysLeuGlnSerIleGlnAlaAsnProGlnAlaArgProThrPheProGly 280
Db 781 ATCAGTCTCATGAGCTCTGCTGGAGAGCCGATCCGAGAGCTGGCGACATTTCTGCGC 840
OY 281 IleGlnGlnLysPheArgProPheTyrLeuSerGlnLeuGlnGlnSerValIleGlnLysP 300
Db 841 ATTGAAGAAAAATTAGCCCTTTTATTATTAAGTCAATTAGAAAGAGTGAAGAGAGAC 900
OY 301 ValLysSerLeuLysGlnTyrSerAsnGlnAsnAlaValValLysArgMetGlnSer 320
Db 901 GTGAAGAGTTTAAAGAAAGATTAATCAAGAAATGCAGTTGTGAAGAGAAATGCAGTCT 960
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OY 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnIlePro 340
Db 961 CTTCACACTGATTTGTGTGGCAGTACTTCAAGCCGGTCAATTTACGCCACAGAACAGCTT 1020
OY 341 GlySerLeuHisSerSerGlnGlyLeuGlnGlyMetGlyProValGlnGlnSerTrpPheAla 360
Db 1021 GGTTCACTGCACAGTCCACAGGAGCTGGATGGTGGTCTGTGAGAGAGTCTGGTTGCTT 1080
OY 361 ProSerLeuGlnHisProGlnGlnGlnLysAsnGlnLysProSerLeuGlnSerLysLeuGlnAsp 380
Db 1081 CCTTCCTCGGAGCACCCCAAGAGAGATGAGCCAGCCCTGCAGAGTAAACTGCAAGAC 1140
OY 381 GlnAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnTrpLysGlnIleProArg 400
Db 1141 GAAGCCAACTGCCATCTTTATGCGACGCCGCTGGACAGCGAGCAAGAAAGACAGCCAG 1200
OY 401 GlnAsnValAlaTyrAsnArgGlnGlnGlnLysArgArgArgValSerHisAspProPhe 420
Db 1201 CAGAAATGGCTTACAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
OY 421 AlaGlnGlnArgProTyrGlnAsnProGlnAsnThrGlnGlyLysGlyThrValTyrSer 440
Db 1261 GCACAGCAAAAGACCTTACGAAATTTTCAGAAATACAGAGGAGGAGGAGGAGGAGGAG 1320
OY 441 SerAlaAlaSerHisGlnLysAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
Db 1321 AGTCGACAGCACTGATGTAATGCAAGTGCACACGCCCTTCAGGGCTTCACAGCCAACTCA 1380
OY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlnPheGlyThrArgProLeuAsp 480
Db 1381 GTACTGATTCAGAAACAAATGATTTATATAGCTACATGGCTTTGGACAGAGCACTGGAT 1440
OY 481 ProGlyThrAlaGlyProArgValTrpTyrArgProIleProSerHisMetProSerLeu 500
Db 1441 CCAGAGACAGAGGCTCCAGAGTTGGTGTGACAGGCCAAATTCAGATCATATCTCAATG 1500
OY 501 HisAsnIleProValProGlnThrAsnTyrLeuGlnLysAsnTrpProThrMetProPheSer 520
Db 1501 CATATATCCAGAGTCCGAGACCACTATGTAGAAATTAACCCACCATCTCCATTCAGC 1560
OY 521 SerLeuProProThrAspGlnSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
Db 1561 TCCTTGGCACCAACAGATGATCTATAAATATACATATACATATAGTACGCTGCTAG 1620
OY 541 IleGlyAlaTyrAsnTyrMetGlnIleGlyGlyThrSerSerSerLeuLeuAspSerThr 560
Db 1621 ATTGAGGCTTCAATTTATATGAGATGTGGTGGAGAGAGTTCATCATCTACTAGACAGCA 1680
OY 561 AsnThrAsnPheLysGlnGlnProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
Db 1681 AATACGAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
OY 581 SerLeuThrAspLysHisLeuAspProIleArgGlnAsnLeuGlnLysHisIleTrpLysAsn 600
Db 1741 AGTCGACAGGATTAACACTGTGACCCCAATACAGGAAATCTGGGAAAGACACTGGAAAAAC 1800
OY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGlnIleAspHisAspTyrGln 620
Db 1801 TGTCCCGCTAAACGGGGCTTTCACACAGTCTGATGATGAATTTGACCAAGCATGATCAG 1860
OY 621 ArgAspGlyLeuLysGlnLysValTyrGlnMetLeuGlnLysTrpValMetArgGlnGly 640
Db 1861 CGAATGACTGAAAGAAAGGTTTACCAGATGCTCCAAAGAGTGGGTGATAGGAGGAGGC 1920
OY 641 IleLysGlyAlaThrIleValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
Db 1921 ATAAAGGAGAGCCAGGTGGGAGAGTGGCCAGGCGCTCCACAGTGTTCAGAGATGCAC 1980
OY 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
Db 1981 CTCTGTGAGCAGCTTGAATTTACGTGACGCCAGAC 2013
```

RESULT 4
 ABN81397
 ID ABN81397 standard; CDNA: 2617 BP.
 AC ABN81397;
 XX
 DT 03-SEP-2002 (first entry)
 DE Human RIP encoding cDNA.
 XX
 KM Human; RIP: cell death protein RIP; receptor interacting protein;
 KM serine/threonine protein kinase; enzyme; immunosuppressive; cardiac;
 KM cerebroprotective; neurotrophic; antiparkinsonian;
 KM virucide; antiarthritic; antirheumatic; antidiabetic; dermatological;
 KM death receptor; caspase; necrosis; immune system; autoimmune disease;
 KM multiple sclerosis; diabetes; rheumatoid arthritis; infection; viral;
 KM neurological disease; Alzheimer's disease; Parkinson's disease; viral;
 KM signal transduction; gene; ss.
 KM
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2016
 FT /tag= a
 FT /product= "RIP"
 XX
 PN WO200236148-A2.
 PD 10-MAY-2002.
 XX
 PF 26-OCT-2001; 2001WO-EP12440.
 XX
 PR 02-NOV-2000; 2000DE-1054279.
 XX
 PA (APOF-) APOTECH RES & DEV LTD.
 PI Tschopp J, Holler N;
 DR WPI: 2002-519224/55.
 DR P-PSDB; ABB83794.
 XX
 PT Use of a death receptor ligand or receptor interacting protein to
 PT induce necrotic cell death, useful for treating e.g. autoimmune
 PT disease, also their inhibitors
 PS
 PS Disclosure; Fig 8: 56pp; German.
 XX
 CC The invention relates to the use of a ligand (I) of the death receptor
 CC or its functional derivative, for inducing caspase-independent (I.e.
 CC necrotic) death (CID) in cells, especially those of the immune system.
 CC (I) are used to induce CID of peripheral blood lymphocytes, especially
 CC activated T cell for treatment of autoimmune diseases. Also CID can be
 CC inhibited by using agents (II) that bind to (I), or agents (III) that
 CC inhibit function of RIP (receptor-interacting protein), particularly for
 CC treatment of autoimmune diseases (e.g. multiple sclerosis, diabetes,
 CC lupus or rheumatoid arthritis); cardiac infarction; cerebral stroke; or
 CC neurological diseases (Alzheimer's or Parkinson's). (III) can also be
 CC used to treat diseases associated, at least in part, with pathological
 CC hypernecrosis and viral infections. The ligand modulates signal
 CC transduction through RIP or the death receptor. The present sequence is
 CC that of the human cell death protein RIP, a serine/threonine kinase,
 CC encoding cDNA of the invention.
 XX
 SO Sequence 2617 BP; 794 A; 586 C; 659 G; 574 T; 4 other;

Alignment Scores:

Pred. No.: 5,88e-264
 Score: 3545.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 24

Length: 2617
 Matches: 671
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-981-397A-16 (1-671) x ABN81397 (1-2617)
 QY
 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
 1 ATGCACACGACATGCTCTTGATGTCATTAAGATGAATCCAGATCTCTCGAGAGT 60
 QY
 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisArgThrGlnGly 40
 61 GCAGAACTGACACGGCGAGGCTTTGGAAAGGTCTCTGTTCCACAGAACCCAGGCA 120
 QY
 41 LeuMetIleMetLysThrValTyrLysGlyProAsnCysIleGluHisAsnGluAlaLeu 60
 121 CTCATGATCATGAAGAAACAGTGTACAAAGGGCCCACTCATTTGACACAAAGAGCCCTC 180
 QY
 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGly 80
 181 TTGGAGAGGCCAATAATGATGACACTTGACACACACGGGTGGTAAAGCTCTGGGC 240
 QY
 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
 241 GTCATCATAGAGAGGAGGAGTACTCCCTGGTGAATGAGTACATGAGAGAGGCAACCTG 300
 QY
 101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleLeu 120
 301 ATGCACGCTGCGAAAGCCGAGATGACTCCGCTTCTGTAAGAGAGATTAATTTTG 360
 QY
 121 GluIleIleGluGluMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
 361 GAATCATTTGAAGAAATGCTGCTACTTACATGAAAAAGCCGCTGATACAAAGACCTGAG 420
 QY
 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
 421 CCTGAATAATATCCTTGATATGATATGATCCATTAAGATGAGCGACCTCGCTTGC 480
 QY
 161 SerPheLysMetThrSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp 180
 481 TCCTTTAAGATGTGGACCAACTGAATATGAAGACCAATAGACTGAGGAATGTGAC 540
 QY
 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAsp 200
 541 GGCACCGCTAAGAAATATGGCGGACCTCTACTACATGAGCGCCGACACCTGATATAC 600
 QY
 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuThrPala 220
 601 CTCACGCAAGCCACAGACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY
 221 IlePheAlaAsnLysGluProThrGluAsnAlaIleCysGluGluGluLeuIleMetLys 240
 661 ATATTTCGAAATTAAGCAGCCATATGAAATCTATCTGTGACACGACCTTGATTAATGTC 720
 QY
 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
 721 ATAAATCTGGGAACAGGCCAGATGTGATGATGATGATGATGATGATGATGATGATG 780
 QY
 261 IleSerLeuMetLysLeuGlyTrpGluAlaAsnProGluAlaArgProThrPheProGly 280
 781 ATCATCTCATGAACCTGCTGCGAAGCAATCCGGAAGCTCGCGCAATTCCTCGC 840
 QY
 281 IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluLysp 300
 841 ATTTGAAGAAAAATTTAGGCTTTTATTTAATCAATTAGAAGAAAGCTGAAGAGGAC 900
 QY
 301 ValLysSerLeuLysGlyLysTyrSerAsnGluAsnAlaValValLysArgMetGlnSer 320
 901 GTGAAGAGTTTAAAGAAAGAGATTCATTAACGAAATGCAAGTTGTGAAGAGATGCACT 960
 QY
 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
 961 CTTCAACTGATTTGTGGACACTTCAACCGCTCAAAATATGACGACAGAACAGCCT 1020
 QY
 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerThrPheAla 360
 1021 GGTTCACGTGACAGTTCCAGGAGCTTGGATGGGCTCTGTGGAGAGAGTCTGTTTCT 1080

QY 361 ProSerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAsp 380
 DB 1081 CCTTCCCTGGAGCACCACAGAGATGACCCACCTGCGAGAGTAACTCCAGAC 1140
 QY 381 GUAAlaasnTyRHisLeuTyRcylSerArgMetAspArgGlnThrLysGlnGlnProArg 400
 DB 1141 GAGCCCACTACATCTTATGGCAGCCGATGAGCAGACGAGAGAAACAGCAGCCGAGA 1200
 QY 401 GlnAsnValAlaTyRAsnArgGluGluGluArgArgArgValSerHisAspProPhe 420
 DB 1201 CAGATGGGCTTCAACAGAGAGAGAGAAAGAGACGAGGCTCCCATGACCCCTTT 1260
 QY 421 AlaGlnGlnArgProTyRAsnArgGlnAsnArgGlnGluGluLysGlyLysGlyThrValTyRser 440
 DB 1261 GCACAGCAAGACCTTACGAGAAATTTCCAGAAATACAGAGGAGGAAAAGCAGCTTTATTC 1320
 QY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
 DB 1321 AGTCAGAGCAGTCAATGTAATGCAAGTCAGCCAGCCCTCAGGGCTCACCAGCAACCTCAA 1380
 QY 461 ValLeuTyRArgHisAsnAsnGlyLeuTyRserSerHisGlyPheGlyThrArgProLeuAsp 480
 DB 1381 GTACTGATCAGAACCAATGATATATAGCTACATGCGCTTGGAAACACACTGAT 1440
 QY 481 ProGlyThrAlaGlyProArgValTrpTyRArgProLeuProSerHisMetProSerLeu 500
 DB 1441 CCAGAGACAGCAGCTCCAGAGTTGGTACAGGCCAATTCAGACATATGCTTGTG 1500
 QY 501 HisAsnLeuProValProGluThrAsnTyRLeuGlyAsnThrProThrMetProPheSer 520
 DB 1501 CATATATCCAGTCCAGTCCAGACCAACTATCTAGAAATFACACCACCATGCAATTCAGC 1560
 QY 521 SerLeuProProThrAspGluSerLysLysTyRThrLysTyRAsnSerThrGlyLysGln 540
 DB 1561 TCCTTGCACCAAGATGATATATAAATATACCAATATCAATAGTACTGCGCATTCAG 1620
 QY 541 IleGlyAlaTyRAsnTyRMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThr 560
 DB 1621 ATTGAGAGCTCAATATATATGAGATTTGGTGGAGCACTTATCCTACTGACAGCA 1680
 QY 561 AsnThrAsnPheLysGluGluProAlaAlaLysTyRAlaAlaPheAspAsnThrThr 580
 DB 1681 AATACGAACCTCAAAAGAGACCAGCTCTAAGTCAAGCAAGCTATCTTGATATATCCACT 1740
 QY 581 SerLeuThrAspLysHisLeuAspProLysArgGluAsnLeuGlyLysHisTrpLysAsn 600
 DB 1741 AGCTGAGGATTAACACCTGACCCCAATCAGGGAATCTGGGAACACTGGAATAAC 1800
 QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyRglu 620
 DB 1801 TGTGCCCTTAACAGTGGCTTCACACAGTCTCAGATTTGTAATTTGACCAATGACATATAG 1860
 QY 621 ArgAspGlyLeuLysGluLysValTyRglnMetLeuGlnLysTrpValMetArgGluGly 640
 DB 1861 CGAGATGAGCTGAAGAAAGATTACAGATGCTCCAAAGTGGGTGATGAGGAGAGGC 1920
 QY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgLysAsp 660
 DB 1921 ATAAAGGAGCCAGGTGGGAGAGCTGGCCACAGGCGCTCCACAGCTGTTCCAGAGATCAG 1980
 QY 661 LeuLeuSerSerLeuIleTyRValSerGlnAsn 671
 DB 1981 CTTCGAGCAGCTGATTTACGTACGCCAGAAC 2013

DE CDNA encoding human cellular kinase RIP protein.
 XX Human: virulence: cytomagalovirus infection; CMV; cellular kinase; RICK;
 KW RIP; Nck-Interacting kinase; MKK3; SRPK-2; gene; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..2016
 FT /tag= a
 FT /product= "Human cellular kinase RIP"
 FN
 PN EPI201765-A2.
 PD 02-MAY-2002.
 XX 15-OCT-2001; 2001EP-0124604.
 PF 16-OCT-2000; 2000US-240750P.
 PR (AXXI-) AXIIMA PHARM AG.
 PA Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
 PI WPI; 2002-373930/41.
 DR P-PSDB; AU080370.
 DR
 XX Identifying agents for treatment or prevention of cytomagalovirus
 PT infection, comprises contacting test compound with cellular kinase and
 PT detecting change in cellular kinase activity
 PS Disclosure: Page 24-27; 49pp; English.
 XX
 CC The present invention relates to a new method for identifying compounds
 CC for treating and/or preventing cytomagalovirus (CMV) infection and/or
 CC related diseases. The method of the invention comprises contacting a
 CC test compound with at least one of the cellular kinases RICK, RIP,
 CC Nck-Interacting kinase, MKK3 and SRPK-2 and detecting any change in
 CC kinase activity. The method of the invention can be used to treat and/or
 CC prevent CMV infections and related diseases. Oligonucleotides that can
 CC detect the specified kinases can also be used for diagnosis of infection.
 CC The present nucleic acid sequence encodes the human cellular kinase RIP
 CC protein of the invention, as described above.
 CC
 SO Sequence 2617 BP: 794 A: 586 C: 659 G: 574 T: 4 other:
 Alignment Scores:
 Pred. No.: 5.88e-264 Length: 2617
 Score: 3545.00 Matches: 671
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-981-397A-16 (1-671) x ABK51170 (1-2617)
 QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGluSer 20
 DB 1 ATGCACACGACATGCTCTTGAATGTCATTAAAGATGAAATCCAGTACTTCTCGAGAGT 60
 QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisArgThrGlnGly 40
 DB 61 GCAGACTGGAGCAGCGAGGCTTGGAGAGGTCTCTGTGTTTCCACAGAACCCAGGGA 120
 QY 41 LeuMetIleMetLysThrValTyRcylProAsnGlyLysGlnGlnGlnGlnGlnGlnGln 60
 DB 121 CTCAATGATCATGAAGAAACAGTGTACAGAGGCGCCCAACTCATTTGAGCAACAGAGCCCTC 180
 QY 61 LeuGlnGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuGlnGly 80
 DB 181 TTGGAGAGCGGAGATGATGAAACAGACTGAGACACAGCCGCGGTGTAACCTCTCGGCG 240
 QY 81 ValIleIleGlnGluGlyLysTyRserLeuValMetGluTyRMetGluLysGlyAsnLeu 100

RESULT 5
 ABK51170
 ID ABK51170 standard: cDNA; 2617 BP.

ABK51170;

30-JUL-2002 (first entry)


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Db 241 GTCATCATAGAGGAAGGAGACTCCCTGGTGGATGGATCATGGAGAGGCAACTG 300
QY 101 MethSVALLLeuValSalGluMetSerThrProLeuSerValLysGlyArgIleLeu 120
Db 301 ATGCACGGTGGAAAGCCGAGATGATCTCCGCTTCTGTAAAAGAGGATTAATTTTG 360
QY 121 GluIleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
Db 361 GAATCATATGGAAGAAATGCTACTACTACATGAAAAAGCCGATACACAGACCTGAG 420
QY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
Db 421 CCTGAAATATCCCTTGTTGATTAATGACTTCCACATTAGATCGCAGACCTCGCCTTCC 480
QY 161 SerPheLysMetIrrPserLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp 180
Db 481 TCCTTTAAGATGTGGAGCAAACTGAATATAGAGCAATGACCTGAGGAACTGGAC 540
QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAsp 200
Db 541 GGCACCGGTAGAGAAATGGCGGACCCCTTACTACTACATGGCGCCGACACCTGATAC 600
QY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValLeuThrPala 220
Db 601 GTCAACGCCAAAGCCACAGAGAAAGTCGATGTACACCTTGGCTGTACTCTGCGCG 660
QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGluLeuLysCys 240
Db 661 ATATTGGAATTAAGAGACCATATGAAATGCTACTGTGAGCAGACACTTATTAATGCG 720
QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
Db 721 ATAAATGTGGGAAGAGCCAGATGTGATGACATCACTGACTACTGCCCAAGAAATT 780
QY 261 IleSerLeuMetLysLeuCysTyrGluAlaAsnProGluAlaArgProThrPheProGly 280
Db 781 ATCATGTCATGAGAGCTCTGCTGGAGAACGATCCGGAAGCTCGGCCACACTTCTCGGC 840
QY 281 IleGluGluLysPheArgProPheTyrLeuSerGluGluGluGluLeuValGluGluAsp 300
Db 841 ATTGAGAGAAAATTAGGCCCTTTTATTATTAAGTCAATTAGAGAAAGTGTAGAAAGAGAC 900
QY 301 ValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValAlaLysArgMetGlnSer 320
Db 901 GTGAAGACTTAAAGAAAGAGATTCACAAAGCAAAATGCAAGTGTCAAGACATGCAAGCT 960
QY 321 LeuGluLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGluPro 340
Db 961 CTTCAACTTGATTTGTGTGGCAGTACTTCAAGCCGGTCAAAATTCAGCCACAGAACAGCCT 1020
QY 341 GlySerLeuHisSerSerGluGlyLeuGlyMetGlyProValGluGluSerThrPheAla 360
Db 1021 GGTTCACCTGCACAGTTCACAGAGACTTGGATGGCTCTGTGGAGAGATCTCGGTTTCT 1080
QY 361 ProSerLeuGluHisProGluGluGluAsnGluProSerLeuGlnSerLysLeuGlnAsp 380
Db 1081 CCTTCCTCCGGAGCACCACCAAGAGAGATGAGCCACCTCGCAGAGTAAACTCCAAAC 1140
QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGluThrLysGluGluProArg 400
Db 1141 GAAGCCCACTACCATCTTATGGCAGCCGATGACAGCAGCAGAAACACAGCCAGCA 1200
QY 401 GlnAsnValAlaTyrAsnArgGluGluGluArgArgArgValSerHisAspProPhe 420
Db 1201 CAGAAATGGCTTACACAGAGAGAGAGAAAGAGACCGAGGCTCCCATGACCTTTT 1260
QY 421 AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSer 440
Db 1261 GCACAGCAAGACCTTACAGAAATTTTCAGAAATACAGAGGGAAGGACACTTATTC 1320
QY 441 SerAlaIleSerHisGlyAsnAlaValHisGluProSerGlyLeuThrSerGluProGln 460
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Db 1321 AGTGACGCCAGTCATGATATATGACAGTGCACACGCCCTCAGGGCTCACACCAACTCA 1380
QY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
Db 1381 GTACTGTATCAGAAACAATGATTTATATAGCTCAGATGGCTTTGGAAACAGCACTGGAT 1440
QY 481 ProGlyThrAlaGlyProArgValTyrPyrArgProIleProSerHisMetProSerLeu 500
Db 1441 CCAGAAACAGCAGTCCCAAGATTGGTACAGGCCAATTCCAAGTCATATCTAGTCTG 1500
QY 501 HisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSer 520
Db 1501 CATATATCCAGTCCAGTCCGAGACCACTATCATAGAAATATACACCACTCCATTCAGC 1560
QY 521 SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
Db 1561 TCCCTGGCACCAACAGATGAATCTATAAAATATACAAATATCAATAGTACTGGCATTCAG 1620
QY 541 IleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThr 560
Db 1621 ATTGAGCCTACAAATATATATGAGATTGGTGGAGAGACTTCACTACTAGACAGCA 1680
QY 561 AsnThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
Db 1681 AATACGAACTTCAAGAGAGAGCCAGCTGCTAAGTATCCAAAGCTATCTTGATAATACCACT 1740
QY 581 SerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisThrLysAsn 600
Db 1741 AGCTGAGCGATTAACACCTGAGCCCAATCAGGGGAAATCTGGGGAACACCTGGAAAAAC 1800
QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGlu 620
Db 1801 TGTGGCCGTAACGTGGCTTCACACAGTCTGAGNTGATGAATTGACACACTATGAG 1860
QY 621 ArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTyrPvalMetArgGluGly 640
Db 1861 CGAGATGAGCTGAAGAAAGGTTTACCAGATGCTCCAAAGTGGTGTATGAGGGAAGGC 1920
QY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
Db 1921 ATAAAGGAGCCAGCGTGGGAGAGCTGGCCAGGGGCTCCACAGTGTCCAGGATGCAC 1980
QY 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
Db 1981 CTTCTGACAGCCTTGATTTAGCTGACGACAGAC 2013

RESULT 6
AAT66408
ID AAT66408 standard; cDNA; 2016 BP.
AC AAT66408;
DT 20-JUL-1997 (first entry)
XX
DE Human receptor interaction protein cDNA.
KW Receptor interaction protein; RIP; tumour necrosis factor;
KW signal transduction; neoplasia; hypersensitivity; inflammation;
KW diagnosis; therapy; ds.
XX
OS Homo sapiens.
XX
PN WO9715586-A1.
PD 01-MAY-1997.
PE 17-OCT-1996; 96WO-US16778.
PF 23-OCT-1995; 95US-0553727.
PR (TULAK-) TULAKIK INC.
PA Baichwal VR, Goeddel DV, Hsu H, Huang J;
PI

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XX WP1: 1997-258948/23.
DR P-PSDB: AAM15461.
XX
XX CDNA encoding human receptor interaction protein or its kinase
PT domain - useful for identifying lead compounds, and for development
PT of therapeutic and diagnostic agents that modulate hrip activity or
PT signal transduction
XX
XX Claim 2: Page 11-13: 22pp; English.
XX
XX A CDNA clone (AAT66408) codes for human receptor interaction protein
CC (RIP) (AAM15461), a novel kinase involved in tumour necrosis factor
CC signal transduction. RIP CDNA can be isolated from a human CDNA
CC libraries (e.g. from umbilical vein endothelial cells) using probes
CC and primers contg. part of the 2016 bp sequence. RIP nucleic acids
CC can be incorporated into cells for expression and screening, or
CC into transgenic animals for functional studies (e.g. the efficacy
CC of candidate drugs for disease associated with expression of RIP).
CC They can also be used as probes e.g. to detect RIP genes and gene
CC transcripts, as primers, in gene therapy applns., and to produce
CC RIP polypeptides (esp. the kinase domain).

SO Sequence 2016 BP: 629 A: 446 C: 515 G: 426 T: 0 other:

Alignment Scores:

Pred. No.: 1-22e-263 Length: 2016
Score: 3539.00 Matches: 670
Percent Similarity: 99.85% Conservative: 0
Best Local Similarity: 99.85% Mismatches: 1
Query Match: 99.83% Indels: 0
DB: 18 Gaps: 0

US-09-981-397a-16 (1-671) x AAT66408 (1-2016)

QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
DB 1 ATGCACACGACATGCTCCTTAATGTCATTAAGATGAATCCAGTCACTTCCTGAGAGT 60
QY 21 AAGlGLeuAspSerGlyGlyPheGlyLysValSerLeuGlySerPheHisArgThrGlnGly 40
DB 61 GCACACTGGACAGGAGGCTTGGAGAGGTCTGTGTGTTCCACAGAACCCAGGA 120
QY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnGlyIleGlnHisAsnGlnAlaLeu 60
DB 121 CTCATGATCATGAAGAACGAGTGAACAGGGCCCACTGATGACACACAGAGCCCTC 180
QY 61 LeuGlnGlnAlaLysMetMetCAsnArgLeuArgHisSerArgValValLysLeuGlnGly 80
DB 181 TTGGAGGAGGCGAGATGATGACAGACTGAGACACACGCGGTGTGTAAGCTCTGGGC 240
QY 81 ValIleIleGlnGlnGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
DB 241 GTCATCATAGAGAGAGAGAGTACTCCCTGGTGGAGGTACATGGAAGAGGCAACCTG 300
QY 101 MetHisValLeuLysAlaGlnMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
DB 301 ATGCACGTGCTGAAGCCGAGATGAGTCTCCGCTTCTGTAAAGAGAGATATTGG 360
QY 121 GluIleIleGlnGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
DB 361 GAAATCATATGGAAGATGCTACTTACATGAAAAGCGTGATGACAAAGACTCTGAAG 420
QY 141 ProGlnAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
DB 421 CCTGAAATATCCTTGTGATTAATGACTCCACATTAAGTGGCAGACCTCGCCTTCC 480
QY 161 SerPheLysMetTyrSerLysLeuAsnAsnGlnGlnHisAsnGlnLeuArgGlnValAsp 180
DB 481 TCCTTAAGATGTGGAGCAAACTGAATATGAAAGCGCAATGAGACTGAGGAATGGAC 540
QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGlnHisLeuAsnAsp 200

DB 541 GGCACCGCTAAGAAAGATGGCGCACCTCTACTACATGAGCGCCGACACCTGAATGAC 600
QY 201 ValAsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValIleuThrAla 220
DB 601 GTCACGCAAGCCACAGAGAGTGGATGTGACACTTGTGTGTACTCTGGGCG 660
QY 221 IlePheAlaAsnLysGlnProTyrGlnAsnAlaIleCysGlnGlnLeuIleMetLys 240
DB 661 ATATTGCAATTAAGAGACCATATGAATGCTATCTGTGAGACACATTCATATATGTC 720
QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGlnIle 260
DB 721 ATAAATCTGGGAGACAGCCAGATGTGATACATCATCTGATCTGCCAAGAGAAAT 780
QY 261 IleSerLeuMetLysLeuGlnGlnGlnAlaAsnProGlnAlaArgProThrPheProGly 280
DB 781 ATCACTCTCATGAACTCTGCTGGGAAACCAATCCGAAAGCTGGCCGACATTTCTTGC 840
QY 281 IleGlnGlnLysPheArgProPheTyrLeuSerGlnLeuGlnGlnSerValGlnGlnAsp 300
DB 841 ATGGAAGAAATTTAGGCCCTTTTATTAGTCAATTAGAAAGAGTGTAGAGAGAC 900
QY 301 ValLysSerLeuLysLysGlnTyrSerAsnGlnAsnAlaValValLysArgMetGlnSer 320
DB 901 GTGAAGACTTTAAGAAAGAGTATTCAAACGAAATGCACTTGTGAAAGATGCACTCT 960
QY 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnGlnPro 340
DB 961 CTTCACTTGAATGTGTGGAGTACCTTCAAGCCGCTCAAAATTCAGCCAGAAACAGCT 1020
QY 341 GlySerLeuHisSerSerGlnGlyLeuGlnMetGlyProValGlnGlnSerThrPheAla 360
DB 1021 GGTTCACCTGCACAGTCCACAGGACTTGGATGGTCTCTGTGGAAGATCCTGGTTTCT 1080
QY 361 ProSerLeuGlnHisProGlnGlnLysAsnGlnProSerLeuGlnSerLysLeuGlnAsp 380
DB 1081 CTTCTCCCTGGAGACCCACAGAAAGAGATGAGCCACCTGACAGATTAACCTCCAGAC 1140
QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
DB 1141 GAAGCCAACTACCATTTTATGAGCAGCCGATGAGCAGGACAGACAAACACAGCCCGA 1200
QY 401 GlnAsnValAlaTyrAsnAsnArgGlnGlnLysArgAsnArgValSerHisAspProPhe 420
DB 1201 CAGAAATGGCTTACAAACAGAGAGAGAAAGAGACAGCCAGGCTCCCATGACCTTTT 1260
QY 421 AlaGlnGlnArgProTyrGlnAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSer 440
DB 1261 GCACAGCAAAAGACCTTACAGAAATTTTCAGAAATACAGAGGGAAGGACACTGTATTC 1320
QY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
DB 1321 AGTCAGCGCATGATGTAATGCACTGACACAGCCCTCAGGGCTTACACAGCCAACTCAA 1380
QY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
DB 1381 GTACTGTATCAGAAACAATGATTAATAGTCACTGACATGGCTTTGGAACAAGACACTGCAT 1440
QY 481 ProGlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeu 500
DB 1441 CCAGGAAACAGAGGCTCCAGAGTTGTGTAAGGCCAATTCCAAGCATATCCTAGTCTG 1500
QY 501 HisAsnIleProValProGlnThrAspTyrLeuGlnGlnAsnThrProThrMetProPheSer 520
DB 1501 CATTAATATCCAGTGTCTGAGACCACTATCTAGGAAATATACACCACCATGCACTTACGC 1560
QY 521 SerLeuProProThrAspGlnSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
DB 1561 TCCTTGCCACCAACAGATGATCTATAAATATATACATATACAAATAGTACGCACTTACG 1620
QY 541 IleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThr 560
DB 1621 ATTGAGCCTTCAATTAATATGAGATGTGTGGAGAGTTCATCATCTAGACAGCAC 1680

QY 561 AsnThrAspPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
DB 1681 AATACGACTTCAAAAGAGAGCCAGCTCTAAGTACCAAGCTATCTTGATTAATACCACT 1740
QY 581 SerLeuThrAspLysHisLeuAspProIleArgIuAsnLeuGlyLysHisTyrPlysAsn 600
DB 1741 AGCTGACGAGTAACACCTGACCCCAATCGAGAAATCTGGAGAACACACTGGAAAC 1800
QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGlu 620
DB 1801 TGTGCCCTTAACCTGGGCTTCACACAGTCTCAGATTGATGAATGACCATGACATGATAG 1860
QY 621 ArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTyrValMetArgGluLys 640
DB 1861 CGAGATGAGACTGAAAGAAAGGTTTACAGATGCTCAAAAGTGGGTGATGAGGAGAGGC 1920
QY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgTlleAsp 660
DB 1921 ATAAAGGAGCCACCGGTGGGAGAGCTGGCCCGCCCTCCACCAAGTGTTCAGAGATCGAC 1980
QY 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
DB 1981 CTTCTGAGCAGCTGATTACTGCTACGACCAAGAAC 2013
RESULT 7
AAT43753
ID AAT43753 standard; cDNA: 2137 BP.
XX AAT43753;
AC AAT43753;
XX 13-FEB-1997 (first entry)
DT
XX
DE Human receptor interacting protein gene.
XX
XX Receptor interacting protein; RIP; cell death; apoptosis;
KW Fas; Apo-1; signal transduction; cancer; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..2016
FT tag= a
FT
XX
PN WO9636730-A1.
XX
XX 21-NOV-1996.
PD
XX
XX 18-APR-1996; 96WO-US05386.
PF
XX
XX 18-MAY-1995; 95US-0444005.
PR
XX
XX (GENO) GEN HOSPITAL CORP.
PA (HARD) HARVARD COLLEGE.
XX
XX Kim E, Leder P, Lee T, Seed B, Stranger BZ;
XX
DR WPI: 1997-012100/01.
XX P-PSDB; AAM04628.
PT
XX Receptor interacting protein having death and kinase domain - useful
PT to control diseases that involve abnormal apoptosis, and for
XX diagnosis and drug screening
XX
PS Disclosure: Page 42-43; 64pp. English.
XX
XX A DNA sequence (AAT43753) codes for human receptor interacting protein
CC (RIP) (AAM04628), a protein that contains a C-terminal death domain
CC through which RIP interacts with the Fas/Apo-1 intracellular domain
CC (ICD). RIP overexpression leads to cell death. The RIP DNA was
CC identified in a yeast two-hybrid screen of a human T-cell cDNA
CC library for proteins that interacted with the Fas/Apo-1 ICD, and by
CC screening a cDNA library with murine RIP cDNA (AAT43752). It can be

CC used as a probe, to produce recombinant RIP in host cells, and in
CC gene therapy either to control the number of cells bearing a
CC specific gene, or to act as an antitumor agent in forms of cancer
CC therapy dependent on delivery of a lethal gene to neoplastic cells.
XX
SQ Sequence 2137 BP; 658 A; 472 C; 550 G; 457 T; 0 other;
Alignment Scores:
Pred. No.: 1,33e-261 Length: 2137
Score: 3513.00 Matches: 666
Percent Similarity: 99.40% Conservative: 1
Best Local Similarity: 99.25% Mismatches: 4
Query Match: 99.10% Indels: 0
DB: 18 Gaps: 0
US-09-981-397a-16 (1-671) x AAT43753 (1-2137)
QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGluSer 20
DB 1 ATGCACCCAGACATGCTCTTCAATGATGATTAAGATGAATCCAGTGACTTCTGAGAGT 60
QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuLysCysPheHisArgThrGlnGly 40
DB 61 GCAGAACTGAGCAGCGGAGGCTTCGCGAAGGTCTCTGTCTTCCACAGAACCCAGGGA 120
QY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnCysIleGluHisAsnGluAlaLeu 60
DB 121 CTCATGATCATGAAMAACAGTGTACAGGGGCCCACTGCAATTGAGCACACAGAGCCCTC 180
QY 61 LeuGluGluAlaLysMetMetLeuAsnArgLeuArgHisSerArgValValLysLeuLeuGly 80
DB 181 TTGGAGAGGCGGAGATGATGATACAGACTGACACACACCGCGGTGGTGAACCTCTTGAGC 240
QY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
DB 241 GTCATCATAGAGGAGGAGAGTACTCCTGTGATGAGGAGCATGAGAGAGGAGCAACCTG 300
QY 101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleLeu 120
DB 301 ATGCACGTGCTGAAGAAGCGAGATGATGCTCTCTCTTCTGAAGAAGAGATATTTTG 360
QY 121 GluIleIleGluGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
DB 361 GAATCATTTGAAGCATGCTCTACTTACATGAAAGCGCTGATACCAAGACCTTGAG 420
QY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
DB 421 CCGTGAATATCTCTTGTGATTAATGACTTCCACATTAAAGATCGCAGACCTGGCCTTGCC 480
QY 161 SerPheLysMetTyrSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp 180
DB 481 TCCTTTAAGATGTGAGCAAACTGATTAATGAGAGCAATGAGCTGAGGAGAGTGAGC 540
QY 181 GlyThrAlaLysLysAsnGlyGlyLysThrLeuTyrTyrMetAlaIleProGluHisLeuAsnAsp 200
DB 541 GCGACCGCTTAAGAAAGTGGCGGACCTCTACTACATGAGGCGCCGAGACCTTAATGAC 600
QY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuTrrAla 220
DB 601 GTCAACGCAAGCCCAACAGAGAGAGTGGATGTGACACTTGTGCTGATGCTCTGGGCG 660
QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGluLeuIleMetCys 240
DB 661 ATATTTCGAATGAGAGAGCATATGAATGCTATCTGTGAGCAGCACTGATTAATGTC 720
QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
DB 721 ATAAATCTGGGAGACAGCCACATGTGATGATGATGATGATGATGATGATGATGATGAT 780
QY 261 IleSerLeuMetLysLeuLysTyrGluAlaAsnProGluAlaArgProThrPheProGly 280
DB 781 ATCAGTCTCATGAACTCTGCTGGGAGAGCAATCCGCAAGCTGGCGGACATTTCTGCGC 840

QY 281 ILeGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAsp 300
 |||||
 Db 841 ATGGAAGAAAAATTAGCCCTTTTATTTAAGTCAATTAGAGAAAGTGTAGAGAGAGAC 900
 |||||
 QY 301 ValIysSerLeuLysGluTyrSerAsnGluAsnAlaValValLysArgMetGluSer 320
 |||||
 Db 901 GTGAGAGATTAAAGAAAGAGATTCAACGAAATTCAGATTGTGAGAGAAATCCAGCT 960
 |||||
 QY 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
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 Db 961 CTTCAACTGATATTGTGGCAGTACTTCAAGCCGGTCAATTCAGCCACAGAAAGAGCT 1020
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 QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTyrPheAla 360
 |||||
 Db 1021 GGTTCACATGCACAGTTCCAGAGGACTTGGATGGGTCTGTGGAGAGTCTGTGTTGGT 1080
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 QY 361 ProSerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGluAsp 380
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 Db 1081 CCTCCCTGGAGCAACCAAGAAAGAAATGAGCCCGCCAGCTCGAGATTAACTCCAGAC 1140
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 QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
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 Db 1141 GAAGCCCACTPACATCTTTATGCGAGCCGATGCGACAGGAGAGAGAAACAGCAGCCAGA 1200
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 QY 401 GlnAsnValAlaTyrAsnArgGluGluGluAlaArgArgArgValSerHisAspProPhe 420
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 Db 1201 CAGATATGGCTTTCACACAGAGAGAGAGAAAGAGAGAGAGGCTCTCCATGACCTTTT 1260
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 QY 421 AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSer 440
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 Db 1261 GCACAGCAAGACCTTACGAGAAATTTTCAGAAATTCAGAGGAGGAAAGGACACTGTTATTC 1320
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 QY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
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 Db 1321 AGTGCACGCCATGATGTAATGACGTCCACCAATCAGGCTCCACAGCAACCTCAA 1380
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 QY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
 |||||
 Db 1381 GTACTGTATCAGAAACATGGATTATATAGCTCAACATGGCTTGGACAAAGACCACTGGAT 1440
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 QY 481 ProGlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeu 500
 |||||
 Db 1441 CCAGGACACAGAGTCCCAAGTTGGTACAGGCCAATTCACATGATATGCCAAGCTG 1500
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 QY 501 HisAsnIleProValProGluThrAsnTyrLeuGlyLysThrProThrMetProPheSer 520
 |||||
 Db 1501 CATTAATATCCAGTGGCTGAGACCACTATCTAGGAATTCCTCCACATGCCATTCAGC 1560
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 QY 521 SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
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 Db 1561 TCCTGGCCACCAACAGATGATCTATAAATATATACATATACATAGTACTGGCATTGAG 1620
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 QY 541 IleGlyAlaTyrAsnTyrMetGluIleGlyLysThrSerSerSerLeuLeuAspSerThr 560
 |||||
 Db 1621 ATTGGACCTACAAATATATGAGAGATTGGTGGAGCGATTCACTACACTAGACAGACACA 1680
 |||||
 QY 561 AsnThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
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 Db 1681 AATAAGCACTTCAAAAGAAAGAGCCAGCTGAAGTACCACTATCTTGAATAATCCACT 1740
 |||||
 QY 581 SerLeuThrAspLysHisLysAspProIleArgGluAsnLeuGlyLysHisTyrLysAsn 600
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 Db 1741 AGTCTGACGATTAACACCTGGACCCCAATCAGGAAAAATCTGGGAAAAAGCCTGGAAAAAC 1800
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 QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluLysPheHisAspTyrGlu 620
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 Db 1801 TGTGCCCGTAAACGTGGCTTCACACAGCTCAGATTGATGAATTCACCATAGCATATGAG 1860
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 QY 621 ArgAspLysLeuLysGluLysValTyrGlnMetLeuGlnLysTyrValMetArgGluGly 640
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 Db 1861 CGGATGAGCTGAAAGAAAGGTTTACCAATGCTCCAAAAGTGGGATGATGAGGAAAGGC 1920
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 QY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
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Db 1921 ATAAAGGAGCCACAGGTGGGAAAGCTGCCAGGCGCTCCACAGCTGTCCAGGATGCGAC 1980
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 QY 661 LeuLeuSerLeuIleTyrValSerGlnAsn 671
 |||||
 Db 1981 CTTCTGAGCAGCTGATTACGTACGACAGAAC 2013
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 RESULT 8
 AAS13810
 ID AAS13810 standard; DNA: 9687 BP.
 XX
 AC AAS13810;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE DNA encoding shuttle vector pPYC.
 DE
 KW Shuttle vector; pPYC; circular; yeast transformation; ds.
 XX
 OS Synthetic.
 XX
 FH Location/Qualifiers
 FH 1..750
 FH promoter
 FT
 FT /tag= a
 FT /note= "Cytomegalovirus (CMV) promoter"
 FT 1158..1662
 FT misc_feature
 FT
 FT /tag= b
 FT /product= "IRES"
 FT /note= "Internal ribosome entry sequence"
 FT 1683..2402
 FT CDS
 FT /tag= c
 FT /product= "GFP"
 FT /note= "Green fluorescent protein"
 FT 2985..4332
 FT misc_feature
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 FT /note= "Yeast 2 mu origin of replication"
 FT 4868..5542
 FT CDS
 FT /tag= e
 FT /product= "TRP"
 FT /note= "Tryptophan"
 FT 5982..6842
 FT CDS
 FT /tag= f
 FT /product= "Beta lactamase"
 FT /note= "Ampicillin resistance"
 FT 7142..7669
 FT misc_feature
 FT
 FT /tag= g
 FT /note= "E. coli origin of replication"
 FT
 PN US6280937-B1.
 XX
 XX 28-AUG-2001.
 PD
 XX
 XX 14-AUG-1998; 98US-0133944.
 PE
 XX
 XX 14-AUG-1998; 98US-0133944.
 PR
 XX
 XX (RIGE-) RIGEL PHARM INC.
 PA
 XX
 XX Luo Y, Yu PW, Lorens J;
 XX
 XX WPI: 2001-588953/66.
 DR
 XX
 XX Screening for a nucleic acid producing a preferred activity or
 FT phenotype in a mammalian cell by transforming yeast with shuttle vector
 FT having an origin of replication, selectable gene, promoter and
 PT homologous recombination site
 PT
 XX
 PS Disclosure: Fig 5; 40pp: English.
 XX
 XX The invention relates to a method of screening for a nucleic acid that
 CC produces a preferred activity or phenotype in a mammalian cell comprising
 CC transforming yeast with a shuttle vector. An advantage of the yeast
 CC system is its efficiency at homologous recombination, and eliminates the

CC steps of manipulating the ends of the vector and the heterologous nucleic
CC acid and ligating the two together. Another advantage is that the yeast
CC can be transformed with large nucleic acids, i.e. up to at least 10 kb,
CC which can then be inserted into the vector. The present sequence
CC represents the coding sequence of shuttle vector pYC used in the
CC method of the invention.

XX Sequence 9687 BP; 2643 A; 2220 C; 2370 G; 2454 T; 0 other;

Alignment Scores:

Pred. No.:	3,9e-260	Length:	9687
Score:	3505.00	Matches:	668
Percent Similarity:	99.70%	Conservative:	0
Best Local Similarity:	99.70%	Mismatches:	2
Query Match:	98.87%	Indels:	1
DB:	22	Gaps:	0

US-09-981-397a-16 (1-671) x AAS13810 (1-9687)

QY 2 GlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSerAla 21
DB 1134 CAACGAGCATGCTCTTGAATGTCATTAAAGATGAATCCAGTACTTCTGGAGAGTGA 1193
QY 22 GluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisArgThrGlnGlyLeu 41
DB 1194 GAACGTGACAGCGGAGGCTTTGGGAAGGTGCTCTGTCTTCCACAGAACCCAGCGACTC 1253
QY 42 MetIleMetLysThrValTyrLysGlyProAsnGlyIleGlnHisAsnGlnAlaLeu 61
DB 1254 ATGATCATGAATAACAGGTGACAGAGGCGCCAACTCATTTGACACACAGAGGCGCTCTTG 1313
QY 62 GlnGlnAlaLysMetMetLeuAsnArgLeuArgHisSerArgValValLysLeuGlnGlyAla 81
DB 1314 GAGGAGCGGAGATGATGATGACAGACTGAGACACAGCCGGGTGAGTCCCTGGGCGTC 1373
QY 82 IleIleGlnGlnGlyLysTyrSerLeuValMetGluTyrMetGlnLysGlnLeuMet 101
DB 1374 ATCATAGAGGAGGAGGAGTACTCCCTGGATGAGTACATGGAAGGCGCAACTGATG 1433
QY 102 HisValLeuLysAlaGlnMetSerThrProLeuSerValLysGlnArgIleIleLeuGln 121
DB 1434 CACGTGCTGAAAGCCGAGATGACTCGCTTCTGTAAAGGAAGGATTAATTGGGGA 1493
QY 122 IleIleGlnGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspPheLeu 141
DB 1494 ATCATTTGAAGGAATGTGCTACTTACATGA -AAGGCGGATGACACAGAGCACTGAAGCTT 1552
QY 142 GlnAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSer 161
DB 1553 GAAATATATCTTGTGATTAATGACTTCCACATTAAAGATCGCAGACCTCGGCTTCCTCC 1612
QY 162 PheLysMetTyrSerLysLeuAsnAsnGlnGlnHisAsnGlnLeuArgGlnValAspGly 181
DB 1613 TTTAAGATGTGAGCAAACTGATTAATGAGAGCCCAATGACTGAGGAAATGGAGGCGC 1672
QY 182 ThrAlaLysLysAsnGlyLysThrLeuTyrTyrMetAlaProGlnHisLeuAsnAspVal 201
DB 1673 ACCGCTAAGAGAATGCGCGCCCTTACTACTGATGCGCCCGAGACCTGAAATGACGTC 1732
QY 202 AsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValValLeuThrAlaIle 221
DB 1733 AACGGAAGCCACAGAGAAAGTGGATGTACAGCTTGTGCTGTACTCTGGGCGATA 1792
QY 222 PheAlaAsnLysGlnProTyrGlnAsnAlaIleCysGlnGlnGlnLeuIleMetCysIle 241
DB 1793 TTTCGAATTAAGGACCATATGAAATGCTATCTGTGACAGCAGACTTGATTAATGTGCATA 1852
QY 242 LysSerGlyAsnArgProAspValAspAspIleThrGlnTyrCysProArgGlnIleIle 261
DB 1853 AAATCTGGGAACAGGCCAGATGTGATGATCATCTACTGAGTACTGCCAAGAAATTTATC 1912
QY 262 SerLeuMetLysLeuCysTyrGlnAlaAsnProGlnAlaArgProThrPheProGlyIle 281
DB 1912

DB 1913 ACTCATGAGACTCTGCTGGAGAGCAATCCGAGAGCTCGCGACATTTCTTGCGATT 1972
QY 282 GlnGlnLysPheArgProPheTyrLeuSerGlnLeuGlnGlnSerValGlnLysAspVal 301
DB 1973 GAGAGAAATTTAGGCTTTTATTTAATGATTAAGAGAAAGTGAAGAGAGAGCTG 2032
QY 302 LysSerLeuLysLysGlnTyrSerAsnGlnAsnAlaValValLysArgMetGlnSerLeu 321
DB 2033 AAGACTTTAAAGAAAGATATTTCAAAGCAAAATGACGTTGTGACAGATGACACTCTT 2092
QY 322 GlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnProGly 341
DB 2213 TCCTCGAGACACCCACAGAGAGATGAGCCGACCTGACAGATTAATCCAGAGCGAA 2272
QY 382 AlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGln 401
DB 2273 GCCAACTACCATCTTTATGGCAGCCGATGACAGCGGAGAGGAGAAACACACCCAGACAG 2332
QY 402 AsnValAlaTyrAsnArgGlnGlnGlnArgArgArgValSerHisAspProPheAla 421
DB 2333 AATGTGCTTACACAGACAGAGAGAGAAAGAGAGCCAGGCTCTCCATGACCTTTTGA 2392
QY 422 GlnGlnArgProTyrGlnAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSerSer 441
DB 2393 CAGCAAAAGACCTTACAGAAATTTTCAGAAATACAGAGGAGAAAGCACGCTTATTCACGT 2452
QY 442 AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnVal 461
DB 2453 GCAGCCACTCATGTGAATGAGTGCAGCCCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCT 2512
QY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
DB 2513 CTGTATCAGAACATAGATTAATATAGCTCATGATGCTTTGGAACAGACCACTGATGCA 2572
QY 482 GlnThrAlaGlyProArgValTyrPyrArgProIleProSerHisMetProSerLeuHis 501
DB 2573 GGAACAGACAGGTCACAGATTTGTGTAACAGGCAATTCAGATCATATCTGATGCTCAT 2632
QY 502 AsnIleProValProGlnThrAsnTyrLeuGlnLysAsnThrProThrMetProPheSerSer 521
DB 2633 AATATCCAGATGCTGAGACCAACATATCTAGAAATACACCCACCATGCTCATTCAGCTCC 2692
QY 522 LeuProProThrAspGlnSerIleLysTyrThrIleTyrAsnSerThrGlyIleGlnIle 541
DB 2693 TTGCCACACACAGATGATCTATAAATATATACATATATAGTACTGCGCATTCAGATT 2752
QY 542 GlnAlaTyrAsnTyrMetGlnIleGlyLysThrSerSerSerLeuLeuAspSerThrAsn 561
DB 2753 GGAGCTTCAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2812
QY 562 ThrAsnPheLysGlnGlnProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSer 581
DB 2813 ACGAACTTCAAGAGAGAGCCAGCTGCTAAGTACAGCAAGCTTCTTGAATAATACACTAGT 2872
QY 582 LeuThrAspLysHisLeuAspProIleArgGlnAsnLeuGlyLysHisTyrLysAsnGly 601
DB 2873 CTGACGAGATTAACACTGAGCCCATTCAGGAAATTCGGGAAACACTGGAAAAACACTGT 2932
QY 602 AlaArgLysLeuGlyPheThrGlnSerGlnIleAspGlnIleAspHisAspTyrGlnArg 621
DB 2933 GCCCGTAAACTGGGCTTACACAGCTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 2992
QY 622 AspGlyLeuLysGlnLysValTyrGlnMetLeuGlnLysTyrPValMetArgGlnGlyIle 641
DB 2993 GATGAGCTGAAAGAAAGTTTACAGATGCTCCAAAAGTGGTGATGAGGAGAGGAGATA 3052

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OY 642 LysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAspLeu 661
DB 3053 AAGGAGCAGCGTGTGGGAGACGTGCCAGCGCTCCACAGATGTTCCAGATCAGCCTT 3112
OY 662 LeuSerSerLeuIleTyrValSerGlnAsn 671
DB 3113 CTGAGCAGCTTGATTTACGTACGACCAAGC 3142

RESULT 9
ABK15129
ID ABK15129 standard; DNA; 9687 BP.
XX
AC ABK15129;
XX
DT 08-MAY-2002 (first entry)
XX
DE Plasmid pPYC.
XX
KW Plasmid; pPYC; transformation; homologous recombination;
XX cyclic; ds.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..750
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FT /label= CMV
FT /note= "Cytomegalovirus"
FT 1158..1662
FT /tag= b
FT /label= IRES
FT /note= "Internal ribosome entry site"
FT 1683..2402
FT /tag= c
FT /product= "GFP"
FT /note= "Green fluorescent protein"
FT 2985..4332
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FT /label= yeast_2micron
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FT /tag= g
FT /note= "Escherichia coli origin of replication"

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PN US2002001830-A1.
XX
PD 03-JAN-2002.
XX
PF 09-DEC-1998; 98US-0208827.
XX
PR 14-AUG-1998; 98US-0133944.
XX
PA (LUOY/) LUO Y.
PA (YUPW/) YU P W.
PA (LORE/) LORENS J.
XX
PI Luo Y, Yu PW, Lorens J;
XX
MP1. 2002-163702/21.
XX
DR Shuttle vector capable of replication in yeast and expression in
XX mammalian cells, useful for transforming yeast, comprises origin of
XX replication and selectable gene functional in yeast and promoter
XX functional in mammalian cell
XX

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PS Example 2: Fig 5A-D; 54pp; English.
XX
CC The invention describes a shuttle vector comprising an origin of
CC replication functional in yeast, a selectable gene functional in yeast,
CC and a promoter functional in a mammalian cell e.g. HeLa cells and capable
CC of directing transcription of a polypeptide coding sequence operably
CC linked downstream from the promoter. The shuttle vector is used to
CC transform yeast. The heterologous nucleic acids are then introduced to
CC the yeast and homologous recombination takes place such that the yeast
CC inserts the heterologous nucleic acid into the shuttle vector at a
CC specific insertion site i.e. a homologous recombination site. The shuttle
CC vectors are then isolated from the yeast and used to transform mammalian
CC cells for expression of the heterologous nucleic acid. The shuttle vector
CC allows exploitation of the yeast two-hybrid system and homologous
CC recombination, and also provides expression in mammalian cells to verify
CC protein-protein interactions, and to study proteins function. This
CC sequence represents the plasmid pPYC, described in the method of the
CC invention.
XX
SQ Sequence 9687 BP; 2643 A; 2220 C; 2370 G; 2454 T; 0 other:

Alignment Scores:
Pred. No.: 3,9e-260 Length: 9687
Score: 3505.00 Matches: 668
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 2
Query Match: 98.87% Indels: 1
DB: 24 Gaps: 0

US-09-981-397A-16 (1-671) x ABK15129 (1-9687)

OY 2. GlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSerAla 21
DB 1134 CAACGACACATGCTCTGATGTCAATTAGAGAAATCCAGAGCTTCTCGAGAGTGCA 1193
OY 22 GlueuAspSerGlyGlyPheGlyLysValSerLeuCysPheHisArgThrGlnIleu 41
DB 1194 GAACGTGACAGCGGAGGCGCTTGGAAAGGTGCTGTGTTGCCAGAACCCAGGAGAC 1253
OY 42 MetIleMetLysThrValTyrIleLysGlyProAsnCysIleGlnHisAsnGlnAlaLeu 61
DB 1254 ATGATCATGAAACAGATGTACAAAGGGCCCACTCATGTGACACACAGGCCCTTTG 1313
OY 62 GlnGluAlaLysMetLeuAsnArgLeuArgHisSerArgValValLysLeuGlnVal 81
DB 1314 GAGGAGCGAAGATATGATGACAGACTGACACACACCGGTGTGTAAAGCTCTGGGCGTC 1373
OY 82 IleIleGlnGlnGlyLysTyrSerLeuValMetGluTyrMetGluLysGlnLysLeuMet 101
DB 1374 ATCATAGAGGAGGAGAGTACCTCGGTGATGGAGTACATGAGAGGCAACCTGATG 1433
OY 102 HisValLeuLysAlaGlnMetSerThrProLeuSerValLysGlyArgIleLeuGln 121
DB 1434 CACGTGCTGAAAGCCGAGATGAGTACCTCGCTTCTGTAAAGGATTAATTTGGGAA 1493
OY 122 IleIleGlnGlnMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysPro 141
DB 1494 ATCATTTGAGGAGATGCTACTTACATGA- AAGGCGTGATACACAGAGACCTTGAAGCT 1552
OY 142 GluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlnLysAsp 161
DB 1553 GAAATATATCCTTGTTGATATATGATCTCCACATTAAAGATCGAGACCTGCTTCCTCC 1612
OY 162 PheLysMetTrpSerLysLeuAsnGlnGluHisAsnGlnLeuArgGlnValAspGly 181
DB 1613 TTTAAGATGTGAGCAACTGAAATATGAGAGCAACATGAGACTGAGGGAATGTGACGCG 1672
OY 182 ThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGlnHisLeuAsnSpVal 201
DB 1673 ACCGCTAAGACAAAGGCGGACCTCTTACTACATGCGGCCGAGACCTGATATACGTC 1732
OY 202 AsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValLeuTrpAlaIle 221

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1733	AACGGAAGGCCACAGAGAAAGTCGAGTGTACAGACTTTCGTGTAGTACTCTGGGCGATA	1792
OY	PheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCysTle	241
Db	TTTGCAAAATTAAGAGGACCATATGAAATGCTATCTGTGTGACGAGCATGTGATATGTGCATA	1852
OY	LysSerGlyAsnArgProAspValAspAspIleThrGlnTyrCysProArgGluIleIle	261
Db	AAATCTGGGAACAGGCCAGATGCTGGATACATCACTAGTACTGCTCCCAAGAAATATATC	1912
OY	SerLeuMetLysLeuCysTTPrgLunAlaAsnProGluAlaArgProThrPheProGlyTle	281
Db	AGTCTCAGAAAGCTCTGCTGTGGAAAGCGAATCCGAAAGTCTGGCCGACATTTCTCCGGCATTT	1972
OY	GluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspVal	301
Db	1973 GAAGAAAATTTAGGCCCTTTTATTATTAAGTCAATTAGCAAGAAAGTGTGGAAGAGACCTG	2032
OY	LysSerLeuLysLysGluTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeu	321
Db	2033 AAGAGTTTAAAGAAAGAGTATTTCACCAAAATCCAGTTGTGAGAGACAATCCACTCTCTT	2092
OY	GlnLeuAspCysValAlaIleProSerSerArgSerAsnSerAlaThrGluGlnProGly	341
Db	2093 CACTTGATGTGTGTGGCAGTACCTTCAAGCCGGTCAAAATTCAGACACAGAACACCTCGGT	2152
OY	SerLeuHisSerSerGlnGluLysMetLysProValGluGluSerTTPheAlaPro	361
Db	2153 TCACCTGCACAGTTCGCCAGGACCTTGGATGGGTCTCTGTGGAGGATCTGTGTTTCTCTCT	2212
OY	SerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLysLysLeuGlnAspGlu	381
Db	2213 TCCCTGGAGCACCCACAAAGAAAGATAGCCGCCAGCTCGAGATTAATCTCCAAAGACGAA	2272
OY	AlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGln	401
Db	2273 GCCAACATGCATCTTATATGGCAGCCGATGGACAGCGACAGAAACAGCACCCACAGACAG	2332
OY	AsnValAlaLysAsnArgGluGluGluArgArgArgValSerHisAspProPheAla	421
Db	2333 AATGGCGCTTCAACACAGAGAGAGAAAGGAGAGCGAGCGTCTCCATGACCTTTGGCA	2392
OY	GlnGlnAlaArgProTyrGluAsnPheGlnAsnThrGlnGluLysGlyThrValTyrSerSer	441
Db	2393 CAGCAAGAACCTTTACGAGAAATTTTCACAGATACAGAGGAAAGACACTGTTATTCACGT	2452
OY	AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnVal	461
Db	2453 GCAGCGAGATCTGTATATGACGTCCACAGCCCTCAGGCGCTCACACAGCAACCTCAAGTA	2512
OY	LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro	481
Db	2513 CTGTATCGAACAATGATTTATATATGCTCACATGGCTTTGGAAACAAGCCACTGTATCCA	2572
OY	GlyThrAlaGlyProArgValTTPryLysArgProIleProSerHisMetProSerLeuHis	501
Db	2573 GGAACAGAGGTCCTCCAGAGTTTGGTAAACAGGCCAATTCANATCATATATGCTCAT	2632
OY	AsnIleProValProGluThrAsnTyrLeuGlnLysAsnThrProThrMetProPheSerSer	521
Db	2633 AATATCCCGAGGCTGTAGACCAACACTATCTAGGAATATACACCACCAATGCCATTCAGCTCC	2692
OY	LeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGluIle	541
Db	2693 TTGGCACCACAGATGATCTATATAATATATACATATACATATACATATAGCTGAGATTCAGATT	2752
OY	GlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThrAsn	561
Db	2753 GGACCCCTCACTATATATGAGATATGGTGGCGAGCTTCATCATCACTACAGACACAAT	2812
OY	ThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSer	581
Db	2813 ACGAATCTCAAGAAAGGACGAGCTGTACAGTACCAAGCTACTCTTGTATTAATACCACTAGT	2872

QY	582	LeuthraspLySHSLeAspPrcITleargLlAsnLeuGLyLysHSTrPLyAsnCys	602
Db	2873	CTGACGAGTAAACACCTTGACACCATCATCAGGAAAATCTGGGAAAAGCACATGGAAAACACTGT	2932
OY	602	AlaarGLyLeuGLyPheThrGLnSerGLnIleaspGLuIleaspHisAspTYrGLuaRG	621
Db	2933	CCCCGTAAACCTGCCTTCACACACTCTCAGATTGATGAAATTTGACCATGTGACTATGACGCA	2992
OY	622	AspGLyLeuLysGLyLysValTYrGLMetLeuGLnLysTrpValMetArgGLuGLyIle	641
Db	2993	GATGGACTGAAAGAAAGATTTCACAGATGCTCCAAAAGTGCGGATGAGGGAAGGATATA	3052
Db	3053	AAGGAGACGACAGTGGGGGGAACCTGGCCAGGCGCTCCACACGATGTTCCAGATCGACCTT	3112
OY	662	LeuSerSerLeuIleTYrValSerGLnAsn	671
Db	3113	CTGAGCAGCTTGATTACGTTCAGCCACGAC	3142
RESULT 10			
AAV99818	ID	AAV99818 standard; cDNA; 3750 BP.	
XX	XX	AAV99818;	
AC	AC		
XX	XX		
DT	DT	12-APR-1999 (first entry)	
XX	XX	Human receptor interacting factor RIF cDNA.	
DE	DE	Receptor interacting protein; RIF; RIF-interacting factor; RIF;	
KW	KW	human; apoptosis; ds.	
KW	KW		
XX	XX	Homo sapiens.	
OS	OS		
XX	XX	Key	Location/Qualifiers
FH	FH	CD5	52..2022
FT	FT		/*tag= a
XX	XX	WO9857985-A2.	
PN	PN		
XX	XX	23-DEC-1998.	
PD	PD		
XX	XX	19-JUN-1998;	98WO-US12778.
PF	PF		
XX	XX	19-JUN-1997;	97US-0050196.
PR	PR		
XX	XX	(CHIR) CHIRON CORP.	
PA	PA		
XX	XX	Shamoon B;	
PI	PI		
XX	XX	WPI. 1999-095325/08.	
DR	DR	P-PSDB; AAW80994.	
XX	XX		
PT	PT	New human RIF-interacting factor - used e.g. to treat muscle	
XX	XX	wasting diseases and autoimmune diseases	
PS	PS	Disclosure: Page 42-44; 57pp; English.	
XX	XX		
CC	CC	This is the nucleotide sequence of cDNA encoding human receptor	
CC	CC	interacting protein (RIF, see AAW80994), a protein involved in the	
CC	CC	Fas-mediated cell death pathway. The invention relates to a novel	
CC	CC	human RIF interacting factor, RIF (see AAW80993) that is involved in	
CC	CC	the regulation of programmed cell death. RIF cDNA (see AAV98817) was	
CC	CC	isolated from a placenta library by two-hybrid analysis with	
CC	CC	murine RIF as bait. Modulation of RIF activity can be used to	
CC	CC	induce or prevent apoptosis, e.g. for the treatment of cancer,	
CC	CC	muscle wasting diseases and autoimmune diseases.	
XX	XX		
50	50	Sequence 3750 BP; 1188 A; 822 C; 919 G; 821 T; 0 other;	

Alignment Scores:

Pred. No.:	6.68e-214	Length:	3750
Score:	2899.00	Matches:	59
Percent Similarity:	53.60%	Conservative:	29
Best Local Similarity:	50.11%	Mismatches:	44
Query Match:	81.76%	Indels:	522
DB:	20	Gaps:	2

US-09-981-397A-16 (1-671) x AAV99818 (1-3750)

OY	1	MetGlnProAspMetSerLeuAsnValIleuysMetLysSerSerAspPheLeuGlnSer	20
Db	52	ATGCACACGACATGTCTCTTGACACATATTAAATGCGATCCAGTACTGTGGAGAG	111
OY	21	AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisArgThrGlnGly	40
Db	112	ACAACTTCAGACAGCGAGCGCTTCGGGAAGGTGTCCTTGTTACCAAGAAACCATGGA	171
OY	41	LeuMetIleMetLysThrValTyrLysGlyProAsnGlyIleGluHisAsnGluAlaLeu	60
Db	172	TTTGTGATCCCGAAAAAGTATTACACAGGGGCCAACCCGCGTGAATACATGAGGTCTTC	231
OY	61	LeuGluGluAlaLysMetMetAsnArgPheLeuArgHisSerArgValValIleuLeuGly	80
Db	232	TTGGAAAGGGGGAAGATGATGATACACAGACTGAGACACACTCGATGTGTAAAGCTACTGGGC	291
OY	81	ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu	100
Db	292	ATTATCATAGAAAGAGGAACCTATTGCGTGTGATGAGTACATGAGAACAGGCAACTG	351
OY	101	MethHisValLeuLysAlaGluMetSerThrProIleuSerValLysGlyArgIleLeu	120
Db	352	ATGCACGGTGTAAAGACCCACATGATGATGCCATTTTCATGTGAAGAGGATATCTGTG	411
OY	121	GluIleIleGluGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys	140
Db	412	GAGCCCATAGAGGCGATGTGCTACTTACATGACAAAGTGATGATACAAAGGACCTGAG	471
OY	141	ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla	160
Db	472	CCTGAGATATCCTCGTGTGATCGTGACTTCCATTAAGATAGCGGATCTTGTTGGCT	531
OY	161	SerPheLysMetTrpSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp	180
Db	532	TCCCTTTAAGACGACGACCAACTACTAAGGAGAAAGCAACAGCAAGAAAGATGACGC	591
OY	181	GlyThrAlaLysLys---AsnGlyGlyThrLeuLysTyrMetAlaProGluHisLeuAsn	199
Db	592	AGCACCCACTAAGAAAGAACATATGTTGGTACCTTTACTACTACATAGGACCCGGAACCTCGAT	651
OY	200	AspValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuTrp	219
Db	652	GACATCAATGAAAGCCGACGGAAGAAGTCCACGCTGACACTTTGGCATGTCTTGG	711
OY	220	AlaIlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGluIleMet	239
Db	712	GCAATATTGCGAAAAAGAGACCCCTATGAGATGTCACTGTACTGAGCAGACTTGTCATC	771
OY	240	CysIleLysSerGlyAsnArgProAspIleAlaAspSerIleThrGlyTyrCysProArgGlu	259
Db	772	TGCTATTAATCTGGGAACAGGCGCAATGTGAAGGAATAATCTTGAGTACTGTCCAAAGGAG	831
OY	260	IleIleSerLeuMetLysLeuCysTyrGluLysAsnProGluAlaArgProThrPhePro	279
Db	832	ATCATCAGCCATCAGAGAGCGGTGCTGGCAGGCGATCCAGAGACAGGCCACACTTTCTT	891
OY	280	GlyIleIleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGlnSerValGluGlu	299
Db	892	GGCATTTGAAGAAATTTAGCCCTTTTACTTAAATGTCATTTTGAAGAAATATGTGAAGAG	951
OY	300	AspVal-----	301
Db	952	GATGT-GCCAACTTTAAAGAAAGATATCCAGATCAAAAGCCGACGTGTCGAGAGAAATTT	1010

QY	301	-----	301
Db	1011	TTCACTCAGCATGACTGTGTATACCTTACCTCCGACGAGTCAATTCAGAAACAACCTGG	1070
QY	301	-----	301
Db	1071	ATCGCTGCAGACTTCCCAAGGGGCTCCAGATGGTCTCTGGAGAGACCTCGTTTCTTC	1130
QY	301	-----	301
Db	1131	CTCCCCAGATACCCACAGACAGAAATGATCGAGTGTGCAGGCTAAGTGCAAAGACA	1190
QY	301	-----	301
Db	1191	AGCCAGCTATCGCTTTTGGAAATTTTGCAGAGAAACAGACAAAACCGACCAAGACA	1250
QY	301	-----	301
Db	1251	GAATGAGCCTTACACACAGAGAGAGAAAGCAAGAGGCTCTCATGACCCCTTTGC	1310
QY	301	-----	301
Db	1311	ACAGCAGAGAGCTGCTGAGAAATTTAAGAGTGCAGAGACAGAGAGTATCTGTATCCAG	1370
QY	301	-----	301
Db	1371	CACAACGAGCTGGAATTCAGTGCACACAGCTGTATGCCACCAACAGATTTC	1430
QY	301	-----	301
Db	1431	GAACATGATGTTATTAATCAAGCATGATTTTGGAACCTACAGTACAGAGATTGGTATCC	1490
QY	301	-----	301
Db	1491	GCCAAATCTAAGCCAAATGATATAGTACTTATAAAACTCCAGTGCAGAGACCAACATACC	1550
QY	301	-----	301
Db	1551	GGGAAGCACACCACACATGATCTCTCTGGGCGATGACAGATGACCTCATAAATA	1610
QY	301	-----	301
Db	1611	TACTATATTCAATAGTTCTGTATTCAGATTGAAACCACTATATATGATGTGGACT	1670
QY	301	-----	301
Db	1671	GAATTCAACACCACCAACATFACTTGCAAAGAAAGTGCAGCTCCAGACACCAAGCAT	1730
QY	301	-----	301
Db	1731	CTTTGATMACCACTAGTGTGACTGATGAACACCTGAAACCTATCAGGAAACCTGG	1790
QY	301	-----	301
Db	1791	AAGCAGTGGAAAACTGTGCCCGCAAGCTGGCTTACTGATGATCGATGAAAT	1850
QY	301	-----	301
Db	1851	CGACCATGACTATGTAAGAGAGATGAGCTGAAGAAAGTTTACCAATGCTTCAGAACTG	1910
QY	301	-----	301
Db	1911	GCTGATGCGGGAAGACCAAAAGGGCCACAGTGGAAAGTTGGCCGAGGACTTCACA	1970
QY	301	-----	301
Db	1971	ATGTTGACAGATAGACCTGCTGAACACATTGATTCGTCCAGCAGAGCTAAGCTGGC	2030
QY	301	-----	301
Db	2031	AGGCTTGCGCAGTGGGAAGCAAACTATTGTCTGTGACACAACCCGTTTGGCCACTAG	2090
QY	301	-----	301

Db 2091 CCTTCAGAGCTATCTCAGCAGTGGCTCTGCAATTTGAGCACAGAGGTCATGCACTTG 2150
 QY 301 ----- 301
 Db 2151 GAAGTGGTGGAGGAAAGACAATCTGAGCCCACTGATTTCTCAGAACATGCAAGCA 2210
 QY 301 ----- 301
 Db 2211 TAAAGCCGCTGATGATGATGCTCGTCATGACCAGTAGAGAAAAAAGCA 2270
 QY 301 ----- 301
 Db 2271 ATACATTAAATACCCGATCTCAGAAATATCAATTAATATATATATATATATATATAT 2330
 QY 301 ----- 301
 Db 2331 GTATTATCTAGAAATATATTACTTACATACACATACCATATATTAGTTCTATTATAGTC 2390
 QY 301 ----- 301
 Db 2391 CACGATTAATCATACGAAGGCGTATCTATCTGTCATCTGTAATACATGGGAGATA 2450
 QY 301 ----- 301
 Db 2451 TGGTAAGAGTGGGTAGTGTGTTGAGAGCTTAAATTTGACGTGGATGAACACTAGCTG 2510
 QY 302 ----- 302
 Db 2511 GAGCTGAAGAGCTTAAAGAAAGAGATATTCAACAGAAATGCAAGTGTGAGAGAGATGAG 2570
 QY 320 SerLeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGln 339
 Db 2571 TCCTTCACCTGATTTGTTGGTGGCACTTCAAGCCGGTCAATTCACGACAGAAACAG 2630
 QY 340 ProGlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGlnSerTyrPhe 359
 Db 2631 CCTGGTTCACCTGACAGAGTCCAGAGGAGTGGGTCTCTGGAGGAGTCTCTGGT 2690
 QY 360 AlaProSerLeuGlnHisProGlnGluGlnAsnGluProSerLeuGlnSerLeuGln 379
 Db 2691 GCTCTCTCCCTGGAGCAGCCCAAGAAAGATAGCCAGCCGTCAGAGTAACCTCAA 2750
 QY 380 AspGluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGln 399
 Db 2751 GACGAGCAAGTACCTCTTATGCGACGCCGATGACAGCAGACGAAACAGACAGCC 2810
 QY 400 ArgGlnAsnValAlaTyrAsnArgGluGluGlnArgArgArgValSerHisAspPro 419
 Db 2811 AGACAGAAATGGCTTACACAGAGAGAGAGAAAGACAGGCTCTCCATGACCT 2870
 QY 420 PheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyr 439
 Db 2871 TTTTCACAGCAAAACCTTACGAGAATTTTCAGAAATACAGAGGAAAAAGCACTTTAT 2930
 QY 440 SerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnPro 459
 Db 2931 TCCAGTCAGAGCACTCATGTATGATGACAGTCACAGCATCAGGCTCACCAGCAACT 2990
 QY 460 GluValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeu 479
 Db 2991 CAACTACTGATTCAGCAAAATGATATATAGCTACATGGCTTTGGAACAGCAACTG 3050
 QY 480 AspProGlyThrAlaGlyProArgValTyrPyrArgProLeuProSerHisMetProSer 499
 Db 3051 GATCAGAGAAACAGAGGCTCCAGAGTTGGTACAGCCCAATTCAGATCATATGCTAGT 3110
 QY 500 LeuHisAsnLeuProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPhe 519
 Db 3111 CTGCATATATATCCAGTGCCTGAGACCAACTATCTAGGAATTTCTCCACCATGCTCAT 3170
 QY 520 SerSerLeuProProThrAspGluSerLeuLysTyrThrIleTyrAsnSerThrGlyIle 539

Db 3171 AGCTCTTGGCCACCACAGATGAATCTATAAATATACATATACATAGTACTGCAAT 3230
 QY 540 GluIleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerLeuLeuAspSer 559
 Db 3231 CAGATTGGAGCCCTCAATTTATATGAGATTGGTGGAGGAGTTCTATCATCTACTAGACAG 3290
 QY 560 ThrAsnThrAsnPhelysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThr 579
 Db 3291 ACAATATCGAACTTCAAGAGAGAGCCAGCTGTAGTACCAACCTATCTTGAATATAC 3350
 QY 580 ThrSerLeuThrAspLysHisLeuAspProIleArgGlnAsnLeuGlyLysHisTyrPlys 599
 Db 3351 ACTAGTCTGAGGATTAACACCTGGACCAATACAGGAAATCTGGGAAAGCACTGGAAA 3410
 QY 600 AsnCysAlaTyrGlyLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyr 619
 Db 3411 AACGTGCCCCCTTAACCTGGGCTTCCACAGTCTCAGTTGATGAATTCACATGACTAT 3470
 QY 620 GluArgAspGlyLeuLysValTyrGlnMetLeuGlnLysTyrPheValMetArgGlu 639
 Db 3471 GAGCGAGATGAGACTGAAGAAAGTTTACCAGATGCTCCAAAAGTGGTGATGAGGAA 3530
 QY 640 GlyIleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIle 659
 Db 3531 GGCATTAAGGAGGAGCCAGGTGGGAGACCTGGCCAGCGCTCCACACAGTCTCCAGATC 3590
 QY 660 AspLeuLeuSerSerLeuIleTyrValSerGlnAsn 671
 Db 3591 GACCTTCTGAGCAGCTTGAATTTTACGTACAGCAGAC 3626
 QY 3591 GACCTTCTGAGCAGCTTGAATTTTACGTACAGCAGAC 3626
 Db 3591 GACCTTCTGAGCAGCTTGAATTTTACGTACAGCAGAC 3626
 RESULT 11
 ID AAT43752 standard; cDNA; 2268 BP.
 AC AAT43752;
 XX AC
 XX AAT43752;
 DT 13-FEB-1997 (first entry)
 DT XX
 DE Mouse receptor interacting protein gene.
 DE XX
 KW Receptor interacting protein; RIP; cell death; apoptosis;
 KW Fas; APO-1; signal transduction; cancer; gene therapy; ss.
 OS Mus sp.
 OS XX
 FH Key Location/Qualifiers
 FT CDS 52..2022
 FT FT /**tag= a
 PN W09636730-A1.
 XX PD
 XX 21-NOV-1996.
 PF 18-APR-1996; 96WO-US05386.
 PF XX
 XX 18-MAY-1995; 95US-0444005.
 PR (GEHO) GEN HOSPITAL CORP.
 PA (HARD) HARVARD COLLEGE.
 PA XX
 FI Kim E, Leder P, Lee T, Seed B, Stranger BZ;
 FI XX
 DR WPI; 1997-012100/01.
 DR P-PSDB; AAM04627.
 DR XX
 FT Receptor interacting protein having death and kinase domain - useful
 FT to control diseases that involve abnormal apoptosis, and for
 FT diagnosis and drug screening
 PS Disclosure; Page 38-39; 64pp; English.
 CC A cDNA clone (AAT43752) codes for mouse receptor interacting protein
 CC (RIP) (AAM04627), a protein which contains a C-terminal death domain

QY 400 ArgGlnAsnValAlaTyrAsnArgGlnGluGluArgArgValSerHisAspPro 419
1246 AGCGAGATGAGGCTTACACAGAGAGAGAAAGAACAGAGGCTCTCATACACC 1305
QY 420 PheAlaGlnGlnArgProTyrGluAsnPhenGlnAsnThrGlnGlyLysGlyThrValTyr 439
1306 TTTTCACAGCAGCAGCTCTGAGAAATATTAAGATGTCAGAGACAGAGATCATCTGAT 1365
QY 440 SerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnPro 459
1366 CCCAGCACACAGAGCTGTCGATTCAGTCAGACAGTCATGCGCCACCCACCA--- 1422
QY 460 GlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeu 479
1423 -----ACAGTTGGACACATGATGTATATATACATGATGATTT----- 1461
QY 480 AspProGlyThrAlaGlyProArgValTyrPyrArgProIleProSerHisMetProSer 499
1462 -----GCACTACAGAGTACAGAGTTGGTATCCGCCAAATCTAAGCAATGATATAGT 1515
QY 500 LeuHisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPhe 519
1516 ACTTATATAAACTCCAGTGCAGAGACCAACATACCGGAGACACACACCATGCCATAC 1575
QY 520 SerSerLeuProProThrAspGluSerIleLeuTyrThrIleTyrAsnSerThrGlyLe 539
1576 TTCCTCGGGCCAGACAGATGACCTCATATAATATATATATATATATATATATATAT 1635
QY 540 GlnIleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSer 559
1636 CAGATTGGAAACCAAT 1683
QY 560 ThrAsnThrAsnPhenGlyGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThr 579
1684 CCANACATACTTGCAGAAAGAGTGCAGCTTCCAGACACCAAGCCATCTTGATATACCC 1743
QY 580 ThrSerLeuThrAspLysHisLeuAspProIleArgGlnAsnLeuGlyLysHisTyrLys 599
1744 ACTAGTGTGATGATGAACACCTGACCTATCAGGAAACCTGCGAAGCAGACGAGAA 1803
QY 600 AsnGlyAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyr 619
1804 AACGTGTGCCCGCAAGCTGGGCTTCACTGAGTCTCAGATCGATGAATCGACCATGACAT 1863
QY 620 GluArgAspGlyLeuLysGlyLysValTyrGlnMetLeuGlnLysTyrValMetArgGlu 639
1864 GAAAGAGATGAGCTGAAAGAGAAAGTTTACCAATGCTTCAGAAAGTGGCTGATGCGGGA 1923
QY 640 GlyIleLysGlyAlaThrValGlyLysLeuAlaGlnAlaValHisGlnCysSerArgIle 659
1924 GGCACCAAGGCGCCACAGTGGGAAAGTGGCCAGAGCATCTTCACCAATGTTCGAGGATA 1983
QY 660 AspLeuLeuSerSerLeuIleTyrValSerGlnAsn 671
1984 GACCTGTGTCAGACCATGTGATTCGTGCCAGCCAGAGC 2019
Db 13-FEB-2002 (first entry)
AA80491 standard; cDNA; 2879 BP.
ID AA80491
AC AA80491
XX 13-FEB-2002 (first entry)
DT DNA encoding novel human diagnostic protein #16295.
DE Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS MO200175067-A2.
PN

XX 11-OCT-2001.
PD 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
PI Dmanac RT, Liu C, Tang YT;
DR WPI: 2001-639362/73.
DR P-PSDB; ABG16304.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
PS Claim 1: SEQ ID No 16295; 103pp; English.
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
CC
SQ Sequence 2879 BP: 751 A: 779 C: 832 G: 517 T: 0 other:
Alignment Scores:
Pred. No.: 1.77e-108 Length: 2879
Score: 1531.00 Matches: 337
Percent Similarity: 64.16% Conservative: 30
Best Local Similarity: 58.92% Mismatches: 99
Query Match: 43.19% Indels: 106
DB: 23 Gaps: 14
US-09-981-397A-16 (1-671) x AAS80491 (1-2879)
QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnUser 20
Db 1234 ATGCACACAGACATGCTCTTAATGTCATTAAGAAATGAAATCAGAGCTTCTGAGAGCT 1293
QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisArgThrGlnGly 40
Db 1294 GCAGACTGACAGCGGAGGCTTTGGAGAGGTCTCTGTGTTTCCACAGAACCCAGGGA 1353
QY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnGlyIleGluHisAsnGluAlaLeu 60
Db 1354 CTCATGATCATGAAGAAACAGTGTACAGAGGCCCACTCATGTGACACACAGAGCCCTC 1413
QY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuGly 80
Db 1414 TTGGAGGAGGCGAAGATGATGAACAGACTGAGACACACCGCGGTGGTAAACCTCCTGGGC 1473
QY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100

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1474 GTCATCATAGAGAGGAGGAGTACTCCCTGGATGGATGATGAGAGAGGACGACCTG 1533
Oy MethisValleuysalaglumetSerThrProleuSerVallysglyArgIlelleu 120
1534 ATGCACGGTGGTGAAGCCGAGATGATGCTCCCTTCTGTAAAGAGATATTTTG 1593
Oy 121 GtullelleuglymetCystTyrLeuHisglYlysglyValleHisLysAspleuLys 140
1594 GAAATCATTTGAAGGAAATGCTACTTACATGAAAAGCGTGAACACAGGACCTGAAG 1653
Oy 141 ProgluasnIleleuValAspAsnAspPheHisIleLysIleala----- 155
1654 CCGTAAATATCTCTGTGATATGACTTCCACATTAGATGAGTACTCCGCTTCTGTA 1713
Oy 155 ----- 155
1714 AAGGAGGATATTTTGGAAATCATTTGAGAGATGCTACTTACATGAAAAGCGCTG 1773
Oy 156 -----AspleuGlyLeuAlaSer-----PheLysMet 164
1774 ATACACAGAGACCTGAGCGTGAATAATCCTTGTGATATGACTTCCACATTAAAGATG 1833
Oy 165 TTPSerLysLeuAsnAsngluHisAsngluLeuArgGluValAspGlyThraLalys 184
1834 TGGACCAATCATATATGAAAGACACATGAGCTGAGGAGAGTGGACCGCTAAG 1893
Oy 185 LysAsnglyGlyThrLeuTyrTyrMetAlaProgluHisLysAsnAspValAsnAlalys 204
1894 AAGAATGGCGGACCCCTACTACTACATGGCGCCGAGCAGCTGAATAGCTCAACGCAAG 1953
Oy 205 ProThrgluLysSerAspValTyrSerPheAlaValleuThrPalalpheAlasn 224
1954 CCCACGAGAGAGCTGGATGTGACAGCTTCTGTAGTACTGTGGCCATATTTGCAAT 2013
Oy 225 LysgluProTyrGluAsnAlaIleCysgluIngluInleuIleMetCysIleLysSerGly 244
2014 AAGGAGCCATATGAAATGCTATCTGTGAGCAGAGCTGATATGATATGCAATAATCTGGG 2073
Oy 245 AsnArgProAspValAspAspIleThrgluTyrCysProArgGluIleleuSerLeuMet 264
2074 AACAGCGCAGATGTGATGACATCACTGACTGCTGCCAAGAAATTTATGCTCATG 2133
Oy 265 LysLeuCysTrpGluAlaAsnProGluAlaArgProThrPhePro----- 279
2134 AACCTGCTGGAAACGATCCGAGAGCTCGGCCACATTCCTGTGGTACAAATTCAG 2193
Oy 280 -----GlyIleGluLysPheArgProPheTyrIleu 290
2194 AACACGCCAAATGGAAGATGATGACAGGCAATTTGAAGAAATTTAGGCCCTTTTATTTA 2253
Oy 291 SerGluLeuGluGluSerValGluGluAspValLysSerLeuLysGluLysSerAsn 310
2254 AGTCATTTTGAAGAAAGTGTAGAGAGAGAGTGAAGAGTTTAAAGCGCCCTTACCTCGCG 2313
Oy 311 GluAsnAlaValLysArgMetGlnSerLeuGluAspCysValAlaValProSer 330
2314 CACCTAGTAAACCCAGAGCGCTACT-----GCCGACCTCGG 2352
Oy 331 SerArg-----SerAsnSerAlaThrGluInProGlySerLeuHisSerGlnGly 348
2353 AACCGAGAGCGCTACTCCCGCCAGCTCGGAACCCAGACCCCTACTCGCGCAC--- 2409
Oy 349 LeuGlyMetGlyProValGluGluSerTrpPheAlaProSerLeuGluHisProGln 368
2410 -----CTCGGAACCCAGAGCCC-----CTACCTGCGCA-----CCTCGGAC 2448
Oy 369 GluAsnGluProSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHisLeuTyrGly 388
2449 CGGAGAGCGCTACCTACCTCGGACCTCGGAACCCAGAGCGCTACCTCGCGCACCTCGGA 2508
Oy 389 SerArgMetAspArgGlnThrLysGlnGluProArgGlnAsnValAlaTyrAsnArgGlu 408
:::

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Db 2509 ACCGACAGAGCGCTACTGCGGACCTCGGACCGCAGAGCGCTACTGCGGACCTCG 2568
Oy 409 GluGluArgArgArgValSerHisAspProPheAlaGlnInlArgProTyrGluAsn 428
Db 2569 GAACCGAGCGCGCTACTGCGGACCTCGGACCGCAGCGCGCTACT----- 2619
Oy 429 PheGlnsnThrGluGluLysGlyThrValTyrSerSerAlaAlaSerHisGlyAsnAla 448
Db 2620 -----GCCGACCTCGGAACCCGACG 2640
Oy 449 ValHisGlnProSerGlyLeuThrSerGlnProGluValleuTyrGlnAsnAsnglyLeu 468
Db 2641 GCG-----CCTACTGCGCGACCTCGGAACCGGCGCCCTACTGCGCGCAC----- 2688
Oy 469 TyrSerSerHisGlyPheGlyThrArg-----ProleuAspProGlyThrAlaGly 485
Db 2689 -----CTCGGAACCGCAGCGCGCTACTGCGGACCTACTGCGGACCTACTAACCAGC 2733
Oy 486 -----ProArgValTrpTyrArgProIleProSerHisMet 497
Db 2734 GCGGCTACTGCGCGGACCTACTGATACCGCAGCGCGCTACTGCGG-----CACCTA 2784
Oy 498 ProSerLeuHisAsnIleProValProGluThrAsn 509
Db 2785 GTAAACCGAGAGCGCTACTGCGGACCTACTGCGGACCTACTGCGGACCTACTGCGG 2820
:::
RESULT 14
AAZ80411
ID AAZ80411 standard; cDNA: 606 BP.
XX
XX AAZ80411;
XX
XX 07-APR-2000 (first entry)
DE Human colon cancer cell line SW480 cDNA clone SEQ ID NO:495.
XX
XX Human; gene expression product; diagnosis; tumour; colon cancer;
XX colorectal adenocarcinoma; cell line SW480; cell proliferation;
XX cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
XX hyperplasia; ds.
XX Homo sapiens.
XX
XX WO964576-A2.
XX
XX 16-DEC-1999.
XX
XX 09-JUN-1999; 99WO-1B01062.
XX
XX 10-JUN-1998; 98US-0088801.
XX
XX (FARB ) BAYER CORP.
XX
XX Endege WO, Steilmann KE, Astle JH, Burgess CC, Bushnell SE;
XX Carroll E, Catino TJ, Derti A, Ford DM, Lewis ME, Monahan JE;
XX Schlegel R;
XX
XX WPI; 2000-087220/07.
XX
XX Novel nucleic acids, used to develop products for the diagnosis and
XX treatment of disorders involving unwanted cell proliferation,
XX particularly cancers, especially colon cancer
XX
XX Claim 15; Page 328; 469pp; English.
XX
XX AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from
XX the human colorectal adenocarcinoma (colon cancer) cell line SW480. The
XX cDNA clones can be used to generate antisense oligonucleotides which
XX can be used for antisense therapy. Methods and products from the present
XX invention can be used for identifying and/or classifying cancerous cells
XX present in a human tumour, particularly in solid tumours, e.g.
XX carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones
XX can be used for developing agents for the diagnosis and treatment of
XX

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CC disorders involving unwanted cell proliferation, such as neoplasia,
CC dysplasia or hyperplasia.

XX Sequence 606 BP; 163 A; 143 C; 158 G; 135 T; 7 other:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 521.00	606	99	0	1	0	0
Percent Similarity: 99.00%						
Best Local Similarity: 99.00%						
Query Match: 14.70%						

US-09-981-397a-16 (1-671) x AA280411 (1-606)

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OY 572 TTTGTLAATLAEHESPSANTHRTTSERLEUTHRASPLYSHTLEUASPROLLEARG 591
    |||||
DB 3 TACCAAGCTATCTTTATATACCACTAGCTACGATTAACACCTGACCAATCAGG 62
    |||||
OY 592 GLUASNLEUGLYLSTRTPLYSASNCYALARGLYLEUGLYPHEHRTGLNSERGLN 611
    |||||
DB 63 GAAATCTGGGAAAGCACTGGAATACTGTCCCTTAACCTGGGCTTCACACACTGCAG 122
    |||||
OY 612 TLEASPGULLEASPHISAPTYGLUARGASDGLYLEULYSGLULYSVALTYRGLMET 631
    |||||
DB 123 ATTGATGAATAATGACATGACTATGAGCGAGATGAGATGAAGAAAGGTTTACAGATG 182
    |||||
OY 632 LLEUGLYLSTRTPLYSALMETARGGLUGLYLLELGLYALATHRYALGLYLSLEUALAGLN 651
    |||||
DB 183 CTCCTCAAAAGTGGTGTGATGAGGAAAGCATTAAGGAGCCAGGCTGGGAAAGCTGGCCAG 242
    |||||
OY 652 ALALEUHSIGLINCYSERARGYLEASPLEULEUSERLEULETYRYVALSERGLNASN 671
    |||||
DB 243 GCGCTCCACAGCTGCTTCGTGATGACCTTCTGACGACCTTCTGACGACCTTCTGACGACGAC 302
    |||||

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RESULT 15

AAK94599 ID AAK94599 standard; cDNA; 1871 BP.

XX AAK94599;

DT 06-NOV-2001 (first entry)

XX Human full-length cDNA, SEQ ID NO: 3541.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

XX EP130094-A2.

XX 05-SEP-2001.

PF 07-JUL-2000; 2000EP-0114089.

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2001-524255/58.

XX P-PSDB; AAM93664.

PT 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
PS Claim 8: SEQ ID NO 3541; 1380BP + sequence listing; English.

XX The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.

XX Sequence 1871 BP; 474 A; 528 C; 516 G; 353 T; 0 other:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 3,47e-26	1871	152	101	187	154	22
Percent Similarity: 42.59%						
Best Local Similarity: 25.59%						
Query Match: 13.02%						

US-09-981-397a-16 (1-671) x AAK94599 (1-1871)

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OY 1 METGLNPROASPMETSERLEUASNVALLLEYS----- 11
    |||
DB 147 CTGGACACCTTCCACCCGATGCTGTGGCTCAAGTATGAGCCACAGGCTGCCGCCGCC 206
    |||
OY 12 METLSSERSEASPHLEUGLUSERLALGLULEU---ASPERGLYGLYPHEGLYLS 30
    |||
DB 207 TTGGTGTCCATTCGACGAACTGGAGAACACGAGAGCTGTGCGCAAGGCGGCTTGGCACA 266
    |||
OY 31 VALSERLEUCSPHEHSARGTHRGINGLYLEUMETLEMETLSTHRYVALTYRGLY 50
    |||
DB 267 GTGTCCGGCGGCAACATAGAGTGGGC-----TAGAGTGTG 305
    |||
OY 51 PROASNCYSLIEGLUHSASNGLUALALEUENGLUGLUALALYSMETLNASARGLEU 70
    |||
DB 306 GCGGTCAAGATTCGTAACCTGMAAGCGATATCCAGGAGGTCAGAGCGCATGGCAAGCTG 365
    |||
OY 71 ARGHISSEARGVALVALYLSLEULEUGLYVALLE-----ILEGLU 85
    |||
DB 366 GATTAACGAATTCGCTGCTGCTAGAGGGGTTATCGAAGAGTGAAGTGGACCAAGAT 425
    |||
OY 86 GLYLSYTSERLEUVALMETGLUTYMETGLULYSLSYLSNLEUMETHSVALLLEULYS 105
    |||
DB 426 CCCAAGCCGGCTGTGACTAAATTCATGAGAACGCGCTCTGTGGGCTGTGCAG 485
    |||
OY 106 ALAGLUMETSERHTRPROLEUSERVALYGLYARGTLEILEUGLUILEILEGLUGLY 125
    |||
DB 486 TCCCAAGTGGCTGGGCGCTGGCGCTCTTTGGCCCTGTGAAGAAGATGGCTTGGG 545
    |||
OY 126 METCYSYTRLEUHSIGLYSGLY-----VALLEHSYLSASPLEULYSPROGLUASN 143
    |||
DB 546 ATGTTTAACTGACGACGACGACGACGACGCTGTGCTGCTGACGCGGACCTCAAGCATCCAC 605
    |||
OY 144 TLEUVALASPSASPHENHSILELSTLEALASPLEUGLYLEUALASERPHLYS 163
    |||
DB 606 GTCTCTGTGAGCCAGCTGCTGCAACCTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTG 665
    |||
OY 164 METTPRESERLYSLEUASNSANGLUGLUNHSASNGLULEUARGGLYTHVALA 183
    |||
DB 666 GGAGGCTACAG-----TCAGGACAGGG 689
    |||
OY 184 LYS---LYSASNGLYLTHRLLEUTYRMETALAPROGLUNHSLEUASNSAPVALASN 202
    |||
DB 690 TCCGGGAGGACGAGGCGACCTGTGCTACTGTGCGCCAGAACGTTTGTAAACGTAAC 749
    |||
OY 203 ALALYSPROTHRGILUSYSEASPYALTYRSEPHALVALYALLEUTPRALALIEPHE 222
    |||
DB 750 CGGAAGGCTCCACAGCAAGTACAGCTTCCGAGTCTTCCAAATGAGGAGTCTT 809
    |||
OY 223 ALASANSYSLU-----PROYRGLU-----ASVALALECYGLU 234
    |||

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Job time : 439 secs

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Db      810 GCTGAGAGAGAGTTGAGTTCACACGAAACATCATCGTGTACGAGACAGTGTCCAAC 869
QY      235 GlnGlnLeuIleMetCysIleIysSerGlyAsnArgProAspValAspAspIleThrGlu 254
Db      870 AGGCAG-----AACGGCCTTCATGGCTGAGCGCCCA 905
QY      255 TyrCysProArgGlu-----IleIleSerLeuMetLysCysTrpGlu 269
Db      906 GCCGGGCTTACAGCTCCCGCTTAGAAGAGCTAGAGAGCTAATGCAGCTCTGTGAGC 965
QY      270 AlaAsnProGluAlaArgProThrPhe-----ProGlyIleGluLysPhe 285
Db      966 AGTGAGCCCAAGACAGACCCCTCTCCAGGAATGCCTACCAAAACTGATGAAGTCTTC 1025
QY      286 ArgProPheTyrLeuSerGlnLeuGlnGluSerValGluGlnAspValLysSerLeuLys 305
Db      1026 CAG-----ATGTGAGAGAACATATGATATGCTGTCTCTCCAGGTAAAG 1070
QY      306 LysGluTyrSerAsnGlnAsnAlaValLysArgMetGlnSerLeuGlnLeuAspCys 325
Db      1071 GATTTCTGTCTCAGCTCAGCAGACAGCAATAGAGATTT----- 1109
QY      326 ValAlaValProSerSerArgSerAsnSerAlaThrGluGlnProGlySerLeuHisSer 345
Db      1110 ---TCTATCCAGAGTCA----- 1124
QY      346 SerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaProSerLeuGlnHis 365
Db      1125 -----GCCCAAGAGGAGACAAATGATGCTTTAGAGAACCATAGAAAAC 1172
QY      366 ProGlnGluLysAsnGluProSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHis 385
Db      1173 CAGCACTCTGTATGATGTCTCATGTCTTGTGAGTGGCTA----- 1211
QY      386 LeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyr 405
Db      1212 -----AACAACTGAATCTAGAGAGCCTCCAGCTCTGTT----- 1247
QY      406 AsnArgGlnGluLysArgArgArgValSerHisAspProPheAlaGlnGlnArgPro 425
Db      1248 -----CTTAAAAATGCCCGAGCCT 1268
QY      426 TyrGlnAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSer-SerAlaAlaSerHis 445
Db      1269 TACCAAGAGGAGGAGGAGCAAGAGAGGAGGTTCCACAGCCTGGACAGCAGCACATC 1328
QY      445 SGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAs 465
Db      1329 TTCAGATTCATGCCCCAACCT-----CCCCAGACTCCAGAGACCTCAACTTTCAG 1379
QY      465 nasnglyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAlaG 485
Db      1380 AACACAGATGCCAGC-----CCTACCTCAACTCGAACCA----- 1413
QY      485 yProArgValTrpTyrArgProIleProSerHisMetProSerLeuHisAsnIleProVa 505
Db      1414 -----CCAAGT-----CCTGG 1424
QY      505 lProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuProProTh 525
Db      1425 ACCCCGAGGAGATCAGGGGCTGAGAGACAAAGCATGAACTGCTCTCCAGAGCCCGGA 1484
QY      525 rAspGluSerIleLys-----TyrThrIleTyrAsnSerThrGlyIleGlnI 541
Db      1485 GCCAAATCCAGTAAACAGGAGGAGCCGCTGTTAAACATATACAACTGCTGGGGGTCAAG 1544
QY      541 eGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSer 554
Db      1545 TGGAGACACAACTACTTGTACTATGCACAGACACTGCC 1584
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Search completed: June 25, 2003, 20:49:20